

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GTAAGCACATGCCTCCAGAGGTGC-3' (SEQ ID NO:426);

reverse PCR primer 5'-GTGACGTGGATGCTTGGGATGTTG-3' (SEQ ID NO:427).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA42801 sequence which had the following nucleotide sequence:

5 hybridization probe

5'-TGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCATTCTGCGTCGA-3' (SEQ ID NO:428).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO731 gene using the probe oligonucleotide and one of the PCR primers. RNA
10 for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255). The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to Sall hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD;
15 pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO731 [herein designated as UNQ395 (DNA48331-1329)] (SEQ ID NO:424) and the derived protein sequence for PRO731.

20 The entire nucleotide sequence of UNQ395 (DNA48331-1329) is shown in Figure 170 (SEQ ID NO:424). Clone UNQ395 (DNA48331-1329) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 329-331 and ending at the stop codon at nucleotide positions 3881-3883 (Figure 170). The predicted polypeptide precursor is 1184 amino acids long (Figure 171). The full-length PRO731 protein shown in Figure 171 has an estimated molecular weight of about 129,022 daltons and
25 a pI of about 5.2. Clone UNQ395 (DNA48331-1329) was deposited with the ATCC on March 31, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO731 polypeptide suggests that portions of it possess significant identity and similarity to members of the protocadherin family, thereby indicating that
30 PRO731 may be a novel protocadherin.

Still analyzing the amino acid sequence of SEQ ID NO:425, the putative signal peptide is at about amino acids 1-13 of SEQ ID NO:425. The transmembrane domain is at amino acids 719-739 of SEQ ID NO:425. The N-glycosylation of SEQ ID NO:425 are as follows: 415-418, 582-586, 659-662, 662-665, and 857-860. The cadherin extracellular repeated domain signatures are at about amino acids (of SEQ ID NO:425): 123-133, 232-
35 242, 340-350, 448-458, and 553-563. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 69: Isolation of cDNA Clones Encoding Human PRO218

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA17411. Two proprietary Genentech EST sequences were employed in the consensus assembly and are shown in Figure 174 and 175. Based on the DNA17411 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO218.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AAGTGGAGCCCGAGCCTTCC-3' (SEQ ID NO:433);

reverse PCR primer 5'-TCGTTGTTTATGCAGTAGTCGG-3' (SEQ ID NO:434).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA17411 sequence which had the following nucleotide sequence:

hybridization probe

5'-ATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGG-3' (SEQ ID NO:435).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO218 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB28).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO218 [herein designated as UNQ192 (DNA30867-1335)] (SEQ ID NO:429) and the derived protein sequence for PRO218.

The entire nucleotide sequence of UNQ192 (DNA30867-1335) is shown in Figure 172 (SEQ ID NO:429). Clone UNQ192 (DNA30867-1335) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 150-152 and ending at the stop codon at nucleotide positions 1515-1517 (Figure 172). The predicted polypeptide precursor is 455 amino acids long (Figure 173). The full-length PRO218 protein shown in Figure 173 has an estimated molecular weight of about 52,917 daltons and a pI of about 9.5. Clone UNQ192 (DNA30867-1335) has been deposited with the ATCC on April 28, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO218 polypeptide suggests that PRO218 may be a novel transmembrane protein.

Still analyzing the amino acid sequence of SEQ ID NO:430, the putative signal peptide is at about amino acids 1 through 23 of SEQ ID NO:430. Transmembrane domains are potentially at about amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, and 425-444 of SEQ ID NO:430. N-glycosylation sites are at about amino acids 67, 180, and 243 of SEQ ID NO:430. Eukaryotic cobalamin-binding protein is at about amino acids 151-160 of SEQ ID NO:430. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 70: Isolation of cDNA Clones Encoding Human PRO768

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43448. Based on the DNA43448 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO768.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GGCTGACACCGCAGTGCTCTTCAG-3' (SEQ ID NO:438);

reverse PCR primer 5'-GCTGCTGGGGACTGCAATGTAGCTG-3' (SEQ ID NO:439).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43448 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATC-3' (SEQ ID NO:440).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO768 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO768 [herein designated as UNQ406 (DNA55737-1345)] (SEQ ID NO:436) and the derived protein sequence for PRO768.

The entire nucleotide sequence of UNQ406 (DNA55737-1345) is shown in Figure 176 (SEQ ID NO:436). Clone UNQ406 (DNA55737-1345) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 20-22 and ending at the stop codon at nucleotide positions 3443-3445 (Figure 176). The predicted polypeptide precursor is 1141 amino acids long (Figure 177). The full-length PRO768 protein shown in Figure 177 has an estimated molecular weight of about 124,671 daltons and a pI of about 5.82. Clone UNQ406 (DNA55737-1345) has been deposited with the ATCC on April 6, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO768 polypeptide suggests that portions of it possess significant sequence identity and similarity with integrin 7.

Still analyzing the amino acid sequence of SEQ ID NO:437, the putative signal peptide is at about amino acids 1-33 of SEQ ID NO:437. The transmembrane domain is at amino acids 1039-1064 of SEQ ID NO:437. N-glycosylation sites are at amino acids: 86-89, 746-749, 949-952, 985-988 and 1005-1008 of SEQ ID NO:437. Integrin alpha chain protein domains are identified at about amino acids: 1064-1071, 384-409, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047 of SEQ ID NO:437. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 71: Isolation of cDNA Clones Encoding Human PRO771

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43330. Based on the DNA43330 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO771.

5 A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CAGCAATATTCAGAAGCGGCAAGGG-3' (SEQ ID NO:443);

reverse PCR primer 5'-CATCATGGTCATCACCCATCATCATC-3' (SEQ ID NO:444).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43330 consensus sequence which had the following nucleotide sequence:

10 hybridization probe

5'-GGTTACTACAAGCCAACACAATGTCATGGCAGTGTGGACAGTGCTGG-3' (SEQ ID NO:445).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO771 gene using the probe oligonucleotide and one of the PCR primers. RNA
15 for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB28).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO771 [herein designated as UNQ409 (DNA49829-1346)] (SEQ ID NO:441) and the derived protein sequence for PRO771.

The entire nucleotide sequence of UNQ409 (DNA49829-1346) is shown in Figure 178 (SEQ ID
20 NO:441). Clone UNQ409 (DNA49829-1346) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 and ending at the stop codon at nucleotide positions 1442-1444 (Figure 178). The predicted polypeptide precursor is 436 amino acids long (Figure 179). The full-length PRO771 protein shown in Figure 179 has an estimated molecular weight of about 49,429 daltons and a pI of about 4.8. Clone UNQ409 (DNA49829-1346) has been deposited with the ATCC on April 7, 1998.
25 Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO771 polypeptide suggests that portions of it possess significant homology to the testican protein, thereby indicating that PRO771 may be a novel testican homologue.

30 Still analyzing the amino acid sequence of SEQ ID NO:442, the putative signal peptide, leucine zipper pattern, N-myristoylation sites, and thyroglobulin type-1 repeats are also shown in Figure 179. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 72: Isolation of cDNA Clones Encoding Human PRO733

35 A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA45600. Based on the DNA45600 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained

the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO733.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCCAGCAGGGATGGGCGACAAGA-3' (SEQ ID NO:448);

reverse PCR primer 5'-GTCTTCCAGTTTCATATCCAATA-3' (SEQ ID NO:449).

- 5 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA45600 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CCAGAAGGAGCACGGGGAAGGGCAGCCAGATCTTGTCGCCCCAT-3' (SEQ ID NO:450).

- 10 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO733 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

- DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO733 [herein designated as UNQ411 (DNA52196-1348)] (SEQ ID NO:446) and the derived protein sequence
15 for PRO733.

- The entire nucleotide sequence of UNQ411 (DNA52196-1348) is shown in Figure 180 (SEQ ID NO:446). Clone UNQ411 (DNA52196-1348) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 106-108 and ending at the stop codon at nucleotide positions 793-795 (Figure 180). The predicted polypeptide precursor is 229 amino acids long (Figure 181). The full-
20 length PRO733 protein shown in Figure 181 has an estimated molecular weight of about 26,017 daltons and a pI of about 4.73. Clone UNQ411 (DNA52196-1348) has been deposited with the ATCC on April 7, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

- Analysis of the amino acid sequence of the full-length PRO733 polypeptide suggests that portions of
25 it possess significant sequence identity and similarity to the T1/ST2 receptor binding protein precursor and therefore may have a similar function in cell signaling. If it is a cytokine, it may be useful in the treatment of inflammation and cancer.

- Still analyzing the amino acid sequence of SEQ ID NO:447, the putative signal peptide, transmembrane domain, N-myristoylation site, and tyrosine kinase site are also shown in Figure 181. The corresponding
30 nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 73: Isolation of cDNA Clones Encoding Human PRO162

- An expressed sequence tag (EST) DNA database (Merck/Washington University) was searched and an EST AA397543 was identified which showed homology to human pancreatitis-associated protein. The EST
35 AA397543 clone was purchased and its insert obtained and sequenced and the sequence obtained is shown in Figure 182 (SEQ ID NO:451).

The entire nucleotide sequence of PRO162 is shown in Figure 182 (SEQ ID NO:451). DNA sequencing of the clone gave the full-length DNA sequence for PRO162 [herein designated as UNQ429 (DNA56965-1356)] (SEQ ID NO:451) and the derived protein sequence for PRO162. Clone UNQ429 (DNA56965-1356) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 86-88 and ending at the stop codon at nucleotide positions 611-613 (Figure 182). The predicted polypeptide precursor is 175 amino acids long (Figure 183). The full-length PRO162 protein shown in Figure 183 has an estimated molecular weight of about 19,330 daltons and a pI of about 7.25. Clone UNQ429 (DNA56965-1356) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO162 polypeptide suggests that portions of it possess significant homology to the human pancreatitis-associated protein, thereby indicating that PRO162 may be a novel pancreatitis-associated protein.

Still analyzing the amino acid sequence of SEQ ID NO:452, the putative signal peptide is at about amino acids 1-26 of SEQ ID NO:452. A C-type lectin domain signature is at about amino acids 146-171 of SEQ ID NO:452. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 74: Isolation of cDNA Clones Encoding Human PRO788

A consensus DNA sequence (designated herein as DNA49308) was assembled relative to other EST sequences using phrap as described in Example 1 above. Based upon an observed homology between the DNA49308 consensus sequence and the Incyte EST clone no. 2777282, the Incyte EST clone no. 2777282 was purchased and its insert obtained and sequenced, which gave the full-length DNA sequence for PRO788 [herein designated as UNQ430 (DNA56405-1357)] (SEQ ID NO:453) and the derived protein sequence for PRO788.

Clone UNQ430 (DNA56405-1357) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 84-86 and ending at the stop codon at nucleotide positions 459-461 (Figure 184). The predicted polypeptide precursor is 125 amino acids long (Figure 185). The full-length PRO788 protein shown in Figure 185 has an estimated molecular weight of about 13,115 daltons and a pI of about 5.90. Clone UNQ430 (DNA56405-1357) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Still analyzing Figure 185, a signal peptide is shown at about amino acids 1-17 of SEQ ID NO:454. An N-glycosylation site is at about amino acids 46-49 of SEQ ID NO:454.

EXAMPLE 75: Isolation of cDNA Clones Encoding Human PRO1008

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated as DNA49804. An EST proprietary to Genentech was employed in the consensus assembly and is herein designated as DNA16508 (Figure 188; SEQ ID NO:457). Based upon an observed homology between the DNA49804 sequence and Merck EST clone no. AA143670, the Merck EST clone no. AA143670 was purchased and its insert obtained and sequenced. That

sequence is shown herein in Figure 186 (SEQ ID NO:455).

Sequencing gave the full length sequence for PRO1008 [herein designated as UNQ492 (DNA57530-1375)] (SEQ ID NO:455) and the derived protein sequence for PRO1008 were identified.

The entire nucleotide sequence of UNQ492 (DNA57530-1375) is shown in Figure 186 (SEQ ID NO:455). Clone UNQ492 (DNA57530-1375) contains a single open reading frame with an apparent
5 translational initiation site at nucleotide positions 138-140 and ending at the stop codon at nucleotide positions 936-938 (Figure 186). The predicted polypeptide precursor is 266 amino acids long (Figure 187). The full-length PRO1008 protein shown in Figure 187 has an estimated molecular weight of about 28,672 daltons and a pI of about 8.85. Clone UNQ492 (DNA57530-1375) has been deposited with the ATCC on May 20, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the
10 sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1008 polypeptide suggests that portions of it possess significant sequence identity and/or similarity with mdck-1, thereby indicating that PRO1008 may be a novel member of this family and have head inducing activity.

Still analyzing the amino acid sequence of SEQ ID NO:456, the putative signal peptide is at about amino
15 acids 1-23 of SEQ ID NO:456. The N-glycosylation site is at about amino acids 256-259 of SEQ ID NO:456, and the fungal zn-(2)-cys(6) binuclear cluster domain is at about amino acids 110-126 of SEQ ID NO:456. The corresponding nucleotides can of all the amino acids can be routinely determined given the sequences provided herein.

20 EXAMPLE 76: Isolation of cDNA Clones Encoding Human PRO1012

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence is herein designated DNA49313. Based on the DNA49313 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for
25 PRO1012.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-ACTCCCCAGGCTGTTCACACTGCC-3' (SEQ ID NO:460);

reverse PCR primer 5'-GATCAGCCAGCCAATACCAGCAGC-3' (SEQ ID NO:461).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA49313 consensus
30 sequence which had the following nucleotide sequence:

hybridization probe

5'-GTGGTGATGATAGAATGCTTTGCCGAATGAAAGGAGTCAACAGCTATCCC-3' (SEQ ID NO:462).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to
35 isolate clones encoding the PRO1012 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1012 [herein designated as UNQ495 (DNA56439-1376)] (SEQ ID NO:458) and the derived protein sequence for PRO1012.

The entire nucleotide sequence of UNQ495 (DNA56439-1376) is shown in Figure 189 (SEQ ID NO:458). Clone UNQ495 (DNA56439-1376) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 404-406 and ending at the stop codon at nucleotide positions 2645-2647 (Figure 189). The predicted polypeptide precursor is 747 amino acids long (Figure 190). The full-length PRO1012 protein shown in Figure 190 has an estimated molecular weight of about 86,127 daltons and a pI of about 7.46. Clone UNQ495 (DNA56439-1376) has been deposited with ATCC on May 14, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1012 polypeptide suggests that portions of it possess sequence identity with disulfide isomerase thereby indicating that PRO1012 may be a novel disulfide isomerase related protein.

Still analyzing the amino acid sequence of SEQ ID NO:459, the cytochrome C family heme-binding site signature is at about amino acids 158-163 of SEQ ID NO:459. The Nt-DNAJ domain signature is at about amino acids 77-96 of SEQ ID NO:459. An N-glycosylation site is at about amino acids 484-487 of SEQ ID NO:459.

The ER targeting sequence is at about amino acids 744-747 of SEQ ID NO:459. It is understood that the polypeptide and nucleic acids disclosed can be routinely formed with or without, these portions as desired, in alternative embodiments. For example, it may be desirable to produce PRO1012 without the ER targeting sequence. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 77: Isolation of cDNA Clones Encoding Human PRO1014

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA49811. Based upon an observed homology between the DNA49811 sequence and Incyte EST clone no. 2612207, Incyte EST clone no. 2612207 was purchased and its insert was obtained and sequenced, wherein the sequence obtained is shown in Figure 191 (SEQ ID NO:463).

DNA sequencing gave the full-length DNA sequence for PRO1014 [herein designated as UNQ497 (DNA56409-1377)] (SEQ ID NO:463) and the derived protein sequence for PRO1014.

The entire nucleotide sequence of UNQ497 (DNA56409-1377) is shown in Figure 191 (SEQ ID NO:463). Clone UNQ497 (DNA56409-1377) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 66-68 and ending at the stop codon at nucleotide positions 966-968 (Figure 191). The predicted polypeptide precursor is 300 amino acids long (Figure 192). The full-length PRO1014 protein shown in Figure 192 has an estimated molecular weight of about 33,655 daltons and a pI of about 9.31. Clone UNQ497 (DNA56409-1377) has been deposited with the ATCC on May 20, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1014 polypeptide suggests that portions of it possess sequence identity with reductase, thereby indicating that PRO1014 may be a novel member of the reductase family.

Still analyzing the amino acid sequence of SEQ ID NO:464, the putative signal peptide is at about amino acids 1-19 of SEQ ID NO:464. The cAMP and cGMP dependent protein kinase phosphorylation sites are at about amino acids 30-33 and 58-61 of SEQ ID NO:464. Short chain alcohol dehydrogenase family proteins are at about amino acids 165-202, 37-49, 112-122 and 210-219 of SEQ ID NO:464. The corresponding nucleotides of these domains and any other amino acids provided herein can be routinely determined given the sequences provided herein.

10 EXAMPLE 78: Isolation of cDNA Clones Encoding Human PRO1017

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein that consensus DNA sequence is herein designated DNA53235. Based upon an observed homology between the DNA53235 consensus sequence and the Merck EST clone no. AA243086, the Merck EST clone no. AA243086 was purchased and its insert obtained and sequenced, wherein the sequence obtained is shown in Figure 193 (SEQ ID NO:465). DNA sequencing gave the full-length DNA sequence for PRO1017 [herein designated as UNQ500 (DNA56112-1379)] (SEQ ID NO:465) and the derived protein sequence for PRO1017.

The entire nucleotide sequence of UNQ500 (DNA56112-1379) is shown in Figure 193 (SEQ ID NO:465). Clone UNQ500 (DNA56112-1379) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 128-130 and ending at the stop codon at nucleotide positions 1370-1372 (Figure 193). The predicted polypeptide precursor is 414 amino acids long (Figure 194). The full-length PRO1017 protein shown in Figure 194 has an estimated molecular weight of about 48,414 daltons and a pI of about 9.54. Clone UNQ500 (DNA56112-1379) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1017 polypeptide suggests that portions of it possess sequence identity with HNK-1 sulfotransferase, thereby indicating that PRO1017 may be a novel sulfotransferase.

Still analyzing the amino acid sequence of SEQ ID NO:466, the putative signal peptide is at about amino acids 1-31 of SEQ ID NO:466. N-glycosylation sites are at about amino acids 134-137, 209-212, 280-283 and 370-273 of SEQ ID NO:466. The TNFR/NGFR family cystein-rich region protein is at about amino acids 329-332 of SEQ ID NO:466. The corresponding nucleotides can be routinely determined given the sequences provided herein. The protein can be secreted.

35 EXAMPLE 79: Isolation of cDNA Clones Encoding Human PRO474

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA49818. Based upon

an observed homology between the DNA49818 consensus sequence and the Merck EST clone no. H77889, the Merck EST clone no. H77889 was purchased and its insert obtained and sequenced, wherein the sequence obtained is herein shown in Figure 195 (SEQ ID NO:467). DNA sequencing gave the full-length DNA sequence for PRO474 [herein designated as UNQ502 (DNA56045-1380)] (SEQ ID NO:467) and the derived protein sequence for PRO474.

5 The entire nucleotide sequence of UNQ502 (DNA56045-1380) is shown in Figure 195 (SEQ ID NO:467). Clone UNQ502 (DNA56045-1380) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 106-108 and ending at the stop codon at nucleotide positions 916-918 (Figure 195). The predicted polypeptide precursor is 270 amino acids long (Figure 196). The full-length PRO474 protein shown in Figure 196 has an estimated molecular weight of about 28,317 daltons and a
10 pI of about 6.0. Clone UNQ502 (DNA56045-1380) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

 Still analyzing the amino acid sequence of SEQ ID NO:468, an N-glycosylation site is at about amino acids 138-141 of SEQ ID NO:468. Short-chain alcohol dehydrogenase family proteins are at about amino acids
15 10-22, 81-91, 134-171 and 176-185 of SEQ ID NO:468. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 80: Isolation of cDNA Clones Encoding Human PRO1031

 An initial consensus DNA sequence was assembled relative to other EST sequences using phrap as
20 described in Example 1 above, wherein the consensus sequence obtained is herein designated as DNA47332. Based upon an observed homology between the DNA47332 sequence and the Merck EST clone no. W74558, Merck EST clone no. W74558 was purchased and its insert obtained and sequenced, wherein the sequence obtained is shown in Figure 197 (SEQ ID NO:469). DNA sequencing gave the full-length DNA sequence for PRO1031 [herein designated as UNQ516 (DNA59294-1381)] (SEQ ID NO:469) and the derived protein
25 sequence for PRO1031.

 The entire nucleotide sequence of UNQ516 (DNA59294-1381) is shown in Figure 197 (SEQ ID NO:469). Clone UNQ516 (DNA59294-1381) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 42-44 and ending at the stop codon at nucleotide positions 582-584 (Figure 197). The predicted polypeptide precursor is 180 amino acids long (Figure 198). The full-length
30 PRO1031 protein shown in Figure 198 has an estimated molecular weight of about 20,437 daltons and a pI of about 9.58. Clone UNQ516 (DNA59294-1381) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

 Analysis of the amino acid sequence of the full-length PRO1031 polypeptide suggests that it is a novel
35 cytokine.

 Still analyzing the amino acid sequence of SEQ ID NO:470, the putative signal peptide is at about amino acids 1-20 of SEQ ID NO:470. An N-glycosylation site is at about amino acids 75-78 of SEQ ID NO:470.

A region having sequence identity with IL-17 is at about amino acids 96-180. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 81: Isolation of cDNA Clones Encoding Human PRO938

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein that consensus sequence is herein designated DNA49798. Based on the DNA49798 DNA consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO938.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GTCCAGCCCATGACCGCCTCCAAC-3' (SEQ ID NO:473)

reverse PCR primer 5'-CTCTCCTCATCCACACCAGCAGCC-3' (SEQ ID NO:474)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA49798 sequence which had the following nucleotide sequence:

hybridization probe

5'-GTGGATGCTGAAATTTTACGCCCCATGGTGTCCATCCTGCCAGC-3' (SEQ ID NO:475)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO938 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO938 [herein designated as UNQ475 (DNA56433-1406)] (SEQ ID NO:471) and the derived protein sequence for PRO938.

The entire nucleotide sequence of UNQ475 (DNA56433-1406) is shown in Figure 199 (SEQ ID NO:471). Clone UNQ475 (DNA56433-1406) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 and ending at the stop codon at nucleotide positions 1181-1183 (Figure 199). The predicted polypeptide precursor is 349 amino acids long (Figure 200). The full-length PRO938 protein shown in Figure 200 has an estimated molecular weight of about 38,952 daltons and a pI of about 4.34. Analysis of the full-length PRO938 sequence shown in Figure 200 (SEQ ID NO:472) evidences the presence of the following features: a signal peptide from amino 1 to about amino acid 22, a transmembrane domain from about amino acid 191 to about amino acid 211, a potential N-glycosylation site from about amino acid 46 to about amino acid 49, a region homologous to disulfide isomerase from about amino acid 56 to about amino acid 72, and a region having sequence identity with flavodoxin proteins from about amino acid 173 to about amino acid 187.

Clone UNQ475 (DNA56433-1406) has been deposited with ATCC on May 12, 1998, and is assigned ATCC Accession No. 209857.

Analysis of the amino acid sequence of the full-length PRO938 polypeptide suggests that it possesses significant sequence similarity to protein disulfide isomerase, thereby indicating that PRO938 may be a novel

protein disulfide isomerase. An analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO938 amino acid sequence and the following Dayhoff sequences, P_W03626, P_W03627, P_R70491, GARP_PLAFF, XLU85970_1, ACADISPROA_1, IE68_HSVSA, KSU52064_1, U93872_83, P_R97866.

5 EXAMPLE 82: Isolation of cDNA Clones Encoding Human PRO1082

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence is herein designated DNA38097. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1082.

10 A set of PCR primers (two forward and one reverse) were synthesized:

forward primer 1 5'-GTCCACAGACAGTCATCTCAGGAGCAG-3' (SEQ ID NO:478);

forward primer 2 5'-ACAAGTGTCTTCCCAACCTG-3' (SEQ ID NO:479);

reverse primer 1 5'-ATCCTCCCAGAGCCATGGTACCTC-3' (SEQ ID NO:480).

15 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA38097 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CCAAGGATAGCTGTTGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCT-3' (SEQ ID NO:481).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primers identified above. A positive library was then used to 20 isolate clones encoding the PRO1082 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1082 [herein designated as UNQ539 (DNA53912-1457)] (SEQ ID NO:476) and the derived protein sequence for PRO1082.

25 The entire nucleotide sequence of UNQ539 (DNA53912-1457) is shown in Figure 201 (SEQ ID NO:476). Clone UNQ539 (DNA53912-1457) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 160-162 and ending at the stop codon at nucleotide positions 763-765 (Figure 201). The predicted polypeptide precursor is 201 amino acids long (Figure 202). The full-length PRO1082 protein shown in Figure 202 has an estimated molecular weight of about 22,563 daltons and a pI of about 4.87. Clone UNQ539 (DNA53912-1457) has been deposited with the ATCC. Regarding the 30 sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

35 Still analyzing the amino acid sequence of SEQ ID NO:477, the transmembrane domain is at about amino acids 45-65 of SEQ ID NO:477. A cAMP- and cGMP-dependent protein kinase phosphorylation site is at about amino acids 197-200 of SEQ ID NO:477. N-myristoylation sites are at about amino acids 35-40 and 151-156 of SEQ ID NO:477. The regions which share sequence identity with the LDL receptor are at about amino acids 34-67 and 70-200 of SEQ ID NO:477. The corresponding nucleotides of these amino acid regions

and others can be routinely determined given the sequences provided herein.

EXAMPLE 83: Isolation of cDNA Clones Encoding Human PRO1083

A cDNA sequence was identified using the amylase screening technique described in Example 2 above, wherein that cDNA sequence is designated herein as DNA24256 (Figure 205; SEQ ID NO:484). That cDNA sequence was then compared and aligned with other known EST sequences as described in Example 1 above to obtain a consensus DNA sequence which is designated herein as DNA43422. Based on the DNA 43422 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1083.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GGCATTGGAGCAGTGCTGGGTG-3' (SEQ ID NO:485);

reverse PCR primer 5'-TGGAGGCCTAGATGCGGCTGGACG-3' (SEQ ID NO:486).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO1083 gene using the reverse PCR primer. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1083 [herein designated as UNQ540 (DNA50921-1458)] (SEQ ID NO:482) and the derived protein sequence for PRO1083.

The entire nucleotide sequence of UNQ540 (DNA50921-1458) is shown in Figure 203 (SEQ ID NO:482). Clone UNQ540 (DNA50921-1458) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 214-216 and ending at the stop codon at nucleotide positions 2293-2295 (Figure 203). The predicted polypeptide precursor is 693 amino acids long (Figure 204). The full-length PRO1083 protein shown in Figure 204 has an estimated molecular weight of about 77,738 daltons and a pI of about 8.87. Clone UNQ540 (DNA50921-1458) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Still analyzing the amino acid sequence of SEQ ID NO:483, the putative signal peptide is at about amino acids 1-25 of SEQ ID NO:483. The transmembrane domains are at about amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590 and 634-657 of SEQ ID NO:483. A microbodies C-terminal targeting signal is at about amino acids 691-693 of SEQ ID NO:483. cAMP- and cGMP-dependent protein kinase phosphorylation sites are at about amino acids 198-201 and 370-373 of SEQ ID NO:483. N-glycosylation sites are at about amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-227 and 341-344 of SEQ ID NO:483. A G-protein coupled receptor family domain is at about amino acids 475-504 of SEQ ID NO:483. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 84: Isolation of cDNA Clones Encoding Human PRO200

Probes based on an expressed sequence tag (EST) identified from the Incyte Pharmaceuticals database due to homology with VEGF were used to screen a cDNA library derived from the human glioma cell line G61. In particular, Incyte Clone "INC1302516" was used to generate the following four probes:

(SEQ ID NO:489) ACTTCTCAGTGTCCTAAGGG;

5 (SEQ ID NO:490) GAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTC;

(SEQ ID NO:491) CACCACAGCGTTTAACCAGG; and

(SEQ ID NO:492) ACAACAGGCACAGTTCCAC.

Nine positives were identified and characterized. Three clones contained the full coding region and were identical in sequence. Partial clones were also identified from a fetal lung library and were identical with
10 the glioma-derived sequence with the exception of one nucleotide change which did not alter the encoded amino acid.

EXAMPLE 85: Expression Constructs for PRO200

For mammalian protein expression, the entire open reading frame (ORF) was cloned into a CMV-based
15 expression vector. An epitope-tag (FLAG, Kodak) and Histidine-tag (His8) were inserted between the ORF and stop codon. VEGF-E-His8 and VEGF-E-FLAG were transfected into human embryonic kidney 293 cells by SuperFect (Qiagen) and pulse-labeled for 3 hours with [³⁵S]methionine and [³⁵C]cysteine. Both epitope-tagged proteins co-migrate when 20 microliters of 15-fold concentrated serum-free conditioned medium were electrophoresed on a polyacrylamide gel (Novex) in sodium dodecyl sulfate sample buffer (SDS-PAGE). The
20 VEGF-E-IgG expression plasmid was constructed by cloning the ORF in front of the human Fc (IgG) sequence.

The VEGF-E-IgG plasmid was co-transfected with Baculogold Baculovirus DNA (Pharmingen) using Lipofectin (GibcoBRL) into 10⁵ Sf9 cells grown in Hink's TNM-FH medium (JRH Biosciences) supplemented with 10% fetal bovine serum. Cells were incubated for 5 days at 28 °C. The supernatant was harvested and subsequently used for the first viral amplification by infecting Sf9 cells at an approximate multiplicity of infection
25 (MOI) of 10. Cells were incubated for 3 days, then supernatant harvested, and expression of the recombinant plasmid determined by binding of 1 ml of supernatant to 30 µl of Protein-A Sepharose CL-4B beads (Pharmacia) followed by subsequent SDS-PAGE analysis. The first amplification supernatant was used to infect a 500 ml spinner culture of Sf9 cells grown in ESF-921 medium (Expression Systems LLC) at an approximate MOI of 0.1. Cells were treated as above, except harvested supernatant was sterile filtered. Specific protein was purified
30 by binding to Protein-A Sepharose 4 Fast Flow (Pharmacia) column.

EXAMPLE 86: Northern Blot Analyses for PRO200

Blots of human poly(A)+ RNA from multiple adult and fetal tissues and tumor cell lines were obtained from Clontech (Palo Alto, CA). Hybridization was carried out using ³²P-labeled probes containing the entire
35 coding region and washed in 0.1 x SSC, 0.1% SDS at 63 °C.

VEGF-E mRNA was detectable in fetal lung, kidney, brain, liver and adult heart, placenta, liver, skeletal muscle, kidney, and pancreas. VEGF-E mRNA was also found in A549 lung adenocarcinoma and HeLa

cervical adenocarcinoma cell lines.

EXAMPLE 87: In Situ Hybridization of Human Fetal Tissue Sections for PRO200

Formalin-fixed, paraffin-embedded human fetal brain, liver, lower limb, small intestine, thyroid, lymph node, thymus, stomach, trachea, skin, spleen, spinal cord, adrenal, placenta, cord, and adult liver, pancreas, lung, spleen, lymph node, adrenal, heart, aorta, and skin were sectioned, deparaffinized, deproteinated in proteinase K (20 μ g/ml) for 15 minutes at 37°C, and further processed for in situ hybridization as described by Lu LH and Gillett NA (Cell Vision 1:169-176, 1994). A [α -³³P]UTP-labeled antisense riboprobe was generated from a PCR product of 980 bp (primers GGCGGAATCCAACCTGAGTAG and GCGGCTATCCTCCTGTGCTC, SEQ ID NOS: 493 and 494, respectively). The slides were dipped in Kodak NTB2 nuclear track emulsion and exposed for 4 weeks.

VEGF-E mRNA expression included localization at the growth plate region and embracing fetal myocytes.

EXAMPLE 88: Myocyte Hypertrophy Assay for PRO200

Myocytes from neonatal Harlan Sprague Dawley rat heart ventricle (23 days gestation) were plated in duplicate at 75000 cells/ml in a 96-well plate. Cells were treated for 48h with 2000, 200, 20, or 2 ng/ml VEGF-E-IgG. Myocytes were stained with crystal violet to visualize morphology and scored on a scale of 3 to 7, 3 being nonstimulated and 7 being full-blown hypertrophy.

2000 ng/ml and 200 ng/ml VEGF-E caused hypertrophy, scored as a 5.

EXAMPLE 89: Cell Proliferation Assay for PRO200

Mouse embryonic fibroblast C3H10T1/2 cells (ATCC) were grown in 50:50 Ham's F-12: low glucose DMEM medium containing 10% fetal calf serum (FCS). Cells were plated in duplicate in a 24-well plate at 1000, 2000, and 4000 cells/well. After 48 hours, cells were switched to medium containing 2% FCS and were incubated for 72 hours with 200, 800, or 2000 ng/ml VEGF-E or no growth factor added.

Approximately 1.5 fold greater number of cells were measured in the presence of 200 ng/ml VEGF-E as in its absence, at all three cell densities.

EXAMPLE 90: Endothelial Cell Survival Assay for PRO200

Human umbilical vein endothelial cells (HUVEC, Cell Systems) were maintained in Complete Media (Cell Systems) and plated in triplicate in serum-free medium (Basic Media from Cell Systems containing 0.1% BSA) at 20,000 cells/well of a 48-well plate. Cells were incubated for 5 days with 200 or 400 ng/ml VEGF-E-IgG, 100 ng/ml VEGF, 20 ng/ml basic FGF, or no addition.

Survival was 2-3 times greater with VEGF-E as compared to lack of growth factor addition. VEGF and basic FGF were included as positive controls.

EXAMPLE 91: Isolation of cDNA Clones Encoding Human PRO285

A proprietary expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched and an EST (#2243209) was identified which showed homology to the *Drosophila* Toll protein.

Based on the EST, a pair of PCR primers (forward and reverse):

5 TAAAGACCCAGCTGTGACCG (SEQ ID NO:499)

ATCCATGAGCCTCTGATGGG (SEQ ID NO: 500), and

a probe:

ATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTC (SEQ ID NO: 501)

were synthesized.

10 mRNA for construction of the cDNA libraries was isolated from human placenta tissue. The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA (Fast Track 2). The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into the cloning vector pCR2.1 (Invitrogen, Inc.)
15 using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). The double stranded cDNA was sized to greater than 1000 bp and the cDNA was cloned into BamHI/NotI cleaved vector. pCR2.1 is a commercially available plasmid, designed for easy cloning of PCR fragments, that carries AmpR and KanR genes for selection, and LacZ gene for blue-white selection.

20 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO285 gene using the probe oligonucleotide and one of the PCR primers.

A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA40021-1154 (encoding PRO285) is shown in Figure 208 (SEQ ID NO:495). Clone DNA40021-1154 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 61-63 (Figure 208). The
25 predicted polypeptide precursor is 1049 amino acids long, including a putative signal peptide at amino acid positions 1-29, a putative transmembrane domain between amino acid positions 837-860, and a leucine zipper pattern at amino acid positions 132-153 and 704-725, respectively. It is noted that the indicated boundaries are approximate, and the actual limits of the indicated regions might differ by a few amino acids. Clone DNA40021-1154 has been deposited with ATCC (designation: DNA40021-1154) and is assigned ATCC deposit no.209389.

30 Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence is a human analogue of the *Drosophila* Toll protein, and is homologous to the following human Toll proteins: Toll1 (DNAX# HSU88540-1, which is identical with the random sequenced full-length cDNA #HUMRSC786-1); Toll2 (DNAX# HSU88878-1); Toll3 (DNAX# HSU88879-1); and Toll4 (DNAX# HSU88880-1).

35

EXAMPLE 92: Isolation of cDNA Clones Encoding Human PRO286

A proprietary expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched and an EST (#694401) was identified which showed homology to the *Drosophila* Toll protein.

Based on the EST, a pair of PCR primers (forward and reverse):

- 5 GCGGAGACAAAAACGTTCTCC (SEQ ID NO:502)
 CATCCATGTTCTCATCCATTAGCC (SEQ ID NO: 503), and

a probe:

TCGACAACCTCATGCAGAGCATCAACCAAAGCAAGAAAACAGTATT (SEQ ID NO: 504)

were synthesized.

- 10 mRNA for construction of the cDNA libraries was isolated from human placenta tissue. This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased
 15 adaptors, cleaved with NotI, sized to greater than 1000 bp appropriately by gel electrophoresis, and cloned in a defined orientation into XhoI/NotI-cleaved pRK5D.

- In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO286 gene using the probe oligonucleotide identified above and one of the PCR
 20 primers.

- A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA42663-1154 (encoding PRO286) is shown in Figure 210 (SEQ ID NO:497). Clone DNA42663-1154 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 57-59 (Figure 211). The predicted polypeptide precursor is 1041 amino acids long, including a putative signal peptide at amino acid
 25 positions 1-26, a potential transmembrane domain at amino acid positions 826-848, and leucine zipper patterns at amino acids 130-151, 206-227, 662-684, 669-690 and 693-614, respectively. It is noted that the indicated boundaries are approximate, and the actual limits of the indicated regions might differ by a few amino acids. Clone DNA42663-1154 has been deposited with ATCC (designation: DNA42663-1154) and is assigned ATCC deposit no. 209386.

- 30 Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence of PRO286, it is a human analogue of the *Drosophila* Toll protein, and is homologous to the following human Toll proteins: Toll1 (DNAX# HSU88540-1, which is identical with the random sequenced full-length cDNA #HUMRSC786-1); Toll2 (DNAX# HSU88878-1); Toll3 (DNAX# HSU88879-1); and Toll4 (DNAX# HSU88880-1).

35

EXAMPLE 93: NF- κ B Assay for PRO285 and PRO286

As the Toll proteins signal through the NF- κ B pathway, their biological activity can be tested in an NF- κ B assay. In this assay Jurkat cells are transiently transfected using Lipofectamine reagent (Gibco BRL) according to the manufacturer's instructions. 1 μ g pB2XLuc plasmid, containing NF- κ B-driven luciferase gene, is cotransfected with 1 μ g pSR α N expression vector with or without the insert encoding PRO285 or PRO286.

- 5 For a positive control, cells are treated with PMA (phorbol myristyl acetate; 20 ng/ml) and PHA (phytohaemagglutinin, 2 μ g/ml) for three to four hours. Cells are lysed 2 or 3 days later for measurement of luciferase activity using reagents from Promega.

EXAMPLE 94: Isolation of cDNA Clones Encoding Human PRO213-1, PRO1330 and PRO1449

- 10 A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA28735. Based on the DNA28735 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO213-1, PRO1330 and/or PRO1449. A pair of PCR primers (forward and reverse) were synthesized:

15 forward PCR primer 5'-TGGAGCAGCAATATGCCAGCC-3' (SEQ ID NO:511)

reverse PCR primer 5'-TTTCCACTCCTGTCGGGTTGG-3' (SEQ ID NO:512)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28735 sequence which had the following nucleotide sequence:

hybridization probe

- 20 5'-GGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGG-3' (SEQ ID NO:513)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO213-1, PRO1330 and/or PRO1449 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue.

- 25 DNA sequencing of the clones isolated as described above gave the full-length DNA sequence encoding PRO213-1, PRO1330 and/or PRO1449 [DNA30943-1-1163-1 (SEQ ID NO:505), DNA64907-1163-1 (SEQ ID NO:507) and DNA64908-1163-1 (SEQ ID NO:509), respectively].

- The entire nucleotide sequences corresponding to DNA30943-1-1163-1 (SEQ ID NO:505), DNA64907-1163-1 (SEQ ID NO:507) and DNA64908-1163-1 (SEQ ID NO:509), respectively. DNA30943-1163, DNA64907-1163-1 and DNA64908-1163-1 contain a single open reading frame with an apparent translational initiation site at nucleotide positions 336-338, 488-490 and 326-328, respectively, and ending at the stop codon at nucleotide positions 1221-1223, 1307-1309 and 1145-1147, respectively (Figures 212, 214 and 216). The predicted polypeptide precursor is 295, 273 and 273 amino acids long, respectively (Figures 213, 215 and 217). DNA30943-1-1163-1, DNA64907-1163-1 and DNA64908-1163-1 have been deposited with ATCC and are assigned ATCC deposit no. 209791, 203242 and 203243, respectively.

Analysis of the amino acid sequence of the full-length PRO213-1 polypeptide suggests that a portion of it possess significant homology to the human growth arrest-specific gene 6 protein. More specifically, an

analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO213 amino acid sequence and the following Dayhoff sequences, HSMHC3W5A_6 and B48089.

Additional analysis of the amino acid sequence of the full-length PRO1330 and PRO1449 polypeptide indicates significant identity with notch4. More specifically, an analysis of the Dayhoff database (version 35.130 SwissProt 35) evidenced significant identity between PRO1330 and the following Dayhoff sequences, D86566_1 and NEL_HUMAN.

EXAMPLE 95: Isolation of cDNA Clones Encoding Human PRO298

A cDNA isolated in the amylase screen described in Example 2 above is herein designated DNA26832 (Figure 220; SEQ ID NO:516). The sequence of DNA26832 was then used to search expressed sequence tag (EST) databases. The EST databases included public EST databases (e.g., GenBank) and a proprietary EST database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266: 469-480 [1996]). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; <http://bozeman.mbt.washington.edu/phrap.docs/phrap.html>).

A consensus DNA sequence was assembled relative to other EST sequences using phrap. A consensus sequence was determined, which was then extended using repeated cycles of BLAST and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above. The extended assembly sequence was designated DNA35861. Based on the DNA35861 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence of PRO298. Forward and reverse primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequence is typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

PCR primers (forward and reverse) and a hybridization probe were synthesized:

forward PCR primer 1 CAACGTGATTTCAAAGCTGGGCTC (SEQ ID NO:517)

forward PCR primer 2 GCCTCGTATCAAGAATTTC (SEQ ID NO:518)

forward PCR primer 3 AGTGGAAGTCGACCTCCC (SEQ ID NO:519)

reverse PCR primer 1 CTCACCTGAAATCTCTCATAGCCC (SEQ ID NO:520)

hybridization probe 1 CGCAAAACCCATTTTGGGAGCAGGAATTCCAATCATGTCTGTGATGGTGG (SEQ ID NO:521)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO298 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB25). The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO298 (herein designated UNQ261 [DNA39975-1210]) (SEQ ID NO:514), and the derived protein sequence for PRO298 (SEQ ID NO:515).

The entire nucleotide sequence of UNQ261 (DNA39975-1210) is shown in Figure 218 (SEQ ID NO:514). Clone DNA39975-1210 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 375-377. The predicted polypeptide precursor is 364 amino acids long. The protein contains four putative transmembrane domains between amino acid positions 36-55 (type II TM), 65-84, 188-208, and 229-245, respectively. A putative N-linked glycosylation site starts at amino acid position 253. In addition, the following features have been identified in the protein sequence: cAMP- and cGMP-dependent protein kinase phosphorylation site, starting at position 8; N-myristoylation sites starting at position 173 and 262, respectively; and a ZP domain between amino acid positions 45-60. Clone DNA39975-1210 has been deposited with ATCC (April 21, 1998) and is assigned ATCC deposit no.209783.

EXAMPLE 96: Isolation of cDNA Clones Encoding Human PRO337

A cDNA sequence identified in the amylase screen described in Example 2 above is herein designated DNA42301 (Figure 223, SEQ ID NO:524). The DNA42301 sequence was then compared to other EST sequences using phrap as described in Example 1 above and a consensus sequence designated herein as DNA28761 was identified. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence. In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO337 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain.

A cDNA clone was sequenced in its entirety. The full length nucleotide sequence of DNA43316-1237 is shown in Figure 221 (SEQ ID NO:522). Clone DNA43316-1237 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 (Figure 221; SEQ ID NO:522). The predicted polypeptide precursor is 344 amino acids long. Clone DNA43316-1237 has been deposited with ATCC and is assigned ATCC deposit no. 209487

Based on a BLAST-2 and FastA sequence alignment analysis of the full-length sequence, PRO337 shows amino acid sequence identity to rat neurotrimin (97%).

EXAMPLE 97: Isolation of cDNA Clones Encoding Human PRO403Introduction:

Human thrombopoietin (THPO) is a glycosylated hormone of 352 amino acids consisting of two domains. The N-terminal domain, sharing 50% similarity to erythropoietin, is responsible for the biological activity. The C-terminal region is required for secretion. The gene for thrombopoietin (THPO) maps to human chromosome 3q27-q28 where the six exons of this gene span 7 kilobase base pairs of genomic DNA (Chang et al., Genomics 26: 636-7 (1995); Foster et al., Proc. Natl. Acad. Sci. USA 91: 13023-7 (1994); Gurney et al., Blood 85: 981-988 (1995). In order to determine whether there were any genes encoding THPO homologues located in close proximity to THPO, genomic DNA fragments from this region were identified and sequenced. Three P1 clones and one PAC clones (Genome Systems Inc., St. Louis, MO; cat. Nos. P1-2535 and PAC-6539) encompassing the THPO locus were isolated and a 140 kb region was sequenced using the ordered shotgun strategy (Chen et al., Genomics 17: 651-656 (1993)), coupled with a PCR-based gap filling approach. Analysis reveals that the region is gene-rich with four additional genes located very close to THPO: tumor necrosis factor-receptor type 1 associated protein 2 (TRAP2) and elongation initiation factor gamma (eIF4), chloride channel 2 (CLCN2) and RNA polymerase II subunit hRPB17. While no THPO homolog was found in the region, four novel genes have been predicted by computer-assisted gene detection (GRAIL)(Xu et al., Gen. Engin. 16: 241-253 (1994), the presence of CpG islands (Cross, S. and Bird, A., Curr. Opin. Genet. & Devel. 5: 109-314 (1995), and homology to known genes (as detected by WU-BLAST2.0)(Altschul and Gish, Methods Enzymol. 266: 460-480 (1996) (<http://blast.wustl.edu/blast/README.html>).

Procedures:P1 and PAC clones:

The initial human P1 clone was isolated from a genomic P1 library (Genome Systems Inc., St. Louis, MO; cat. no.: P1-2535) screened with PCR primers designed from the THPO genomic sequence (A.L. Gurney, et al., Blood 85: 981-88 (1995). PCR primers were designed from the end sequences derived from this P1 clone were then used to screen P1 and PAC libraries (Genome Systems, Cat. Nos.: P1-2535 & PAC-6539) to identify overlapping clones (PAC1, p1.t, and P1.u). The 3'-end sequence from PAC.z was used to define the primers used for the screening of a human BAC library (Genome Systems Inc., St. Louis, MO; Cat. No.: BDTW-4533A).

Ordered Shotgun Strategy:

The Ordered Shotgun Strategy (OSS) (Chen et al., Genomics 17: 651-656 (1993)) involves the mapping and sequencing of large genomic DNA clones with a hierarchical approach. The P1 or PAC clone was sonicated and the fragments subcloned into lambda vector (λ BlueStar) (Novagen, Inc., Madison, WI; cat. no. 69242-3). The lambda subclone inserts were isolated by long-range PCR (Barnes, W. Proc. Natl. Acad. Sci. USA 91: 2216-2220 (1994) and the ends sequenced. The lambda-end sequences were overlapped to create a partial map of the original clone. Those lambda clones with overlapping end-sequences were identified, the insets subcloned into a plasmid vector (pUC18 or pUC19, Hoefer Pharmacia Biotech, Inc., San Francisco, CA, Cat. Nos. 27-4949-01 and 27-4951-01) and the ends of the plasmid subclones were sequenced and assembled to generate a contiguous sequence. This directed sequencing strategy minimizes the redundancy required while allowing one

to scan for and concentrate on interesting regions.

In order to define better the THPO locus and to search for other genes related to the hematopoietin family, five genomic clones were isolated from this region by PCR screening of human P1 and PAC libraries (Genome System, Inc., Cat. Nos.: P1-2535 and PAC-6539).

The sizes of the genomic fragments are as follows: P1.t is 40 kb; P1.g is 70 kb; P1.u is 70 kb; PAC.z is 200 kb; and BAC.1 is 80 kb. Approximately 75% (140 kb) of the 190 kb genomic DNA region was sequenced by the Ordered Shotgun Strategy (OSS) (Chen et al., Genomics 17: 651-56 (1993), and assembled into contigs using AutoAssemblerTM (Applied Biosystems, Perkin Elmer, Foster City, CA, cat. no. 903227). The preliminary order of these contigs was determined by manual analysis. There were 47 contigs the 140 kb region. A PCR-based approach to ordering the contigs and filling in the gaps was employed. The following summarizes the number and sizes of the gaps. The 50 kb of sequence unique to BAC.1 was sequenced by a total shotgun approach with a ten-fold redundancy.

<u>Size of gap</u>	<u>number</u>
< 50 bp	13
50-150 bp	7
150-300 bp	7
300-1000 bp	10
1000-5000 bp	7
> 5000 bp	2 ((15,000 bp)

20 DNA sequencing:

ABI DYE-primerTM chemistry (PE Applied Biosystems, Foster City, CA; Cat. No.: 402112) was used to end-sequence the lambda and plasmid subclones. ABI DYE-terminaterTM chemistry (PE Applied Biosystems, Foster City, CA, Cat. No: 403044) was used to sequence the PCR products with their respective PCR primers. The sequences were collected with an ABI377 instrument. For PCR products larger than 1kb, walking primers were used. The sequences of contigs generated by the OSS strategy in AutoAssemblerTM (PE Applied Biosystems, Foster City, CA; Cat. No: 903227) and the gap-filling sequencing trace files were imported into SequencherTM (Gene Codes Corp., Ann Arbor, MI) for overlapping and editing. The sequences generated by the total shotgun strategy were assembled using Phred and Phrap and edited using Consed (<http://chimera.biotech.washington.edu/uwgc/projects.htm>) and GFP (Genome Reconstruction Manager for Phrap), version 1.2 (<http://stork.cellb.bcm.tmc.edu/gfp/>).

PCR-Based gap filling Strategy:

Primers were designed based on the 5'- and 3'-end sequenced of each contig, avoiding repetitive and low quality sequence regions. All primers were designed to be 19-24-mers with 50-70% G/C content. Oligos were synthesized and gel-purified by standard methods.

Since the orientation and order of the contigs were unknown, permutations of the primers were used in the amplification reactions. Two PCR kits were used: first, XL PCR kit (Perkin Elmer, Norwalk, CT; Cat. No.: N8080205), with extension times of approximately 10 minutes; and second, the Taq polymerase PCR kit

(Qiagen Inc., Valencia, CA; Cat. No.: 201223) was used under high stringency conditions if smeared or multiple products were observed with the XL PCR kit. The main PCR product from each successful reaction was extracted from a 0.9% low melting agarose gel and purified with the GeneClean DNA Purification kit prior to sequencing.

Analysis:

- 5 The identification and characterization of coding regions was carried out as follows: First, repetitive sequences were masked using RepeatMasker (A.F.A. Smit & P. Green, http://ftp.genome.washington.edu/RM/RM_details.html) which screens DNA sequences in FastA format against a library of repetitive elements and returns a masked query sequence. Repeats not masked were identified by comparing the sequence to the GenBank database using WUBLAST2.0 [Altschul, S & Gish, W., Methods
10 Enzymol. 266: 460-480 (1996); <http://blast.wustl.edu/blast/README.html>] and were masked manually.

Next, known genes were revealed by comparing the genomic regions against Genentech's protein database using the WUBLAST2.0 algorithm and then annotated by aligning the genomic and cDNA sequences for each gene, respectively, using a Needleman-Wunch (Needleman and Wunsch, J. Mol. Biol. 48: 443-453 (1970) algorithm to find regions of local identity between sequences. The strategy results in detection of all
15 exons of the five known genes in the region, THPO, TRAP2, eIF4g, CLCN2 and hRPB17 (see below).

<u>Known genes</u>	<u>Map position</u>
eukaryotic translation initiation factor 4 gamma	3q27-qter
thrombopoietin	3q26-q27
20 chloride channel 2	3q26-qter
TNF receptor associated protein 2	not previously mapped
RNA polymerase II subunit hRPB17	not previously mapped

- Finally, novel transcription units were predicted using a number of approaches. CpG islands (S. Cross
25 & Bird, A., Curr. Opin. Genet. Dev. 5: 109-314 (1995) islands were used to define promoter regions and were identified as clusters of sites cleaved by enzymes recognizing GC-rich, 6 or 8-mer palindromic sequences (NotI, NarI, BssHII, XhoI. CpG islands are usually associated with promoter regions of genes. WUBLAST2.0 analysis of short genomic regions (10-20 kb) versus GenBank revealed matches to ESTs. The individual EST sequences (or where possible, their sequence chromatogram files) were retrieved and assembled with Sequencer
30 to provide a theoretical cDNA sequence (DNA36443). GRAIL2 (ApoCom Inc., Knoxville, TN, command line version for the DEC alpha) was used to predict a novel exon. The five known genes in the region served as internal controls for the success of the GRAIL algorithm.

Isolation:

- A partial endothelin converting enzyme-2 (ECE-2) cDNA clone was isolated by first splicing in silico
35 the ECE-2 exons predicted in the genomic sequence to generate a putative sequence (DNA36443). An oligonucleotide probe: GAAGCAGTGCAGCCAGCAGTAGAGAGGCACCTGCTAAGA) (SEQ ID NO:530) was designed and used to screen a human fetal small intestine library (LIB110) and internal PCR primers

(36443f1) (ECE2.f:ACGCAGCTGGAGCTGGTCTTAGCA) (SEQ ID NO:531) and (36443r1) (ECE2.r) (GGTACTGGACCCCTAGGGCCACAA) (SEQ ID NO:532) were used to confirm clones hybridizing to the probe prior to sequencing. One positive clone was obtained, however this cDNA (DNA49830) represented a partially spliced transcript containing appropriately spliced exons 1 through 6, followed by intron 6 sequence. The oligo dT primer annealed to a polyA-stretch within an Alu element present in intron 6. An additional ECE-2
 5 cDNA fragment (DNA49831) was obtained by PCR from a human fetal kidney library (LIB227) with primers designed from the presumed cDNA sequence [36443f3: CCTCCCAGCCGAGACCAGTGG (SEQ ID NO:533) and 36443r2: GGTCTATAAGGGCCAAGACC (SEQ ID NO:534)]. This PCR product extended from exon 13 into the 3' untranslated region in exon 18.

A full length endothelin converting enzyme 2 (ECE-2) cDNA clone (DNA55800-1263) was isolated
 10 from an oligo-dT-primed human fetal brain library. RNA from human fetal brain tissue (20 weeks gestation, #283005)(SRC175) was isolated by guanidine thiocyanate and 5 μ g used to generate double stranded cDNA which was cloned into the vector pRK5E. The 3' -primer (pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTTT) (SEQ ID NO:535) and the 5 -linker (pCGGACGCGTGGGTCGA) (SEQ ID NO:536) were designed to introduce XhoI and NotI restriction sites.
 15 The library was screened with PCR primers [36443pcrf1: CGGCCGTGATGGCTGGTGACG (SEQ ID NO:537) and 36443r3: GGCAGACTCCTTCCTATGGG (SEQ ID NO:538)] designed from the partial human ECE-2 cDNA sequences (DNA49830 and DNA49831). PCR products were cloned into the vector pCR2.1-TOPO (Invitrogen Corp., Carlsbad, CA, Cat. No. K4500-01) and sequenced with DYE-terminator chemistry as described above.

20

EXAMPLE 98: Northern Blot and in situ RNA Hybridization Analysis for PRO403

Expression of PRO403 mRNA in human tissues was examined by Northern blot analysis. Human polyA+ RNA blots derived from human fetal and adult tissues (Clontech, Palo Alto, CA; Cat. Nos. 7760-1, 7756-1 and 7755-1) were hybridized to a [32P- α]dATP-labelled cDNA fragments from probe based on the full
 25 length PRO403 cDNA. Blots were incubated with the probes in hybridization buffer (5X SSPE; 2X Denhardt's solution; 100 mg/mL denatured sheared salmon sperm DNA; 50% formamide; 2% SDS) for 18 hours at 42°C, washed to high stringency (0.1XSSC, 0.1% SDS, 50°C) and autoradiographed. The blots were developed after overnight exposure by phosphorimager analysis (Fuji).

PRO403 mRNA transcripts were detected. Analysis of the expression pattern showed the strongest
 30 signal of the expected 3.3 kb transcript in adult brain (highest in the cerebellum, putamen, medulla, and temporal lobe, and lower in the cerebral cortex, occipital lobe and frontal lobe), spinal cord, lung and pancreas and higher levels of a 4.5 kb transcript in fetal brain and kidney.

EXAMPLE 99: Use of PRO Polypeptide-Encoding Nucleic Acid as Hybridization Probes

35 The following method describes use of a nucleotide sequence encoding a PRO polypeptide as a hybridization probe.

DNA comprising the coding sequence of of a PRO polypeptide of interest as disclosed herein may be employed as a probe or used as a basis from which to prepare probes to screen for homologous DNAs (such as those encoding naturally-occurring variants of the PRO polypeptide) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO polypeptide-encoding nucleic acid-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO polypeptide can then be identified using standard techniques known in the art.

EXAMPLE 100: Expression of PRO Polypeptides in *E. coli*

This example illustrates preparation of an unglycosylated form of a desired PRO polypeptide by recombinant expression in *E. coli*.

The DNA sequence encoding the desired PRO polypeptide is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the specific PRO polypeptide coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO polypeptide can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO181, PRO195, PRO200, PRO237, PRO273, PRO540, PRO322, PRO1017, PRO938, PRO162, PRO1114, PRO827 and PRO1008 were expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding the PRO polypeptide was initially amplified using selected PCR primers. The

primers contained restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences were then ligated into an expression vector, which was used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants were first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.₆₀₀ of 3-5 was reached. Cultures were then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate·2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples were removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets were frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) was resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution was stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution was centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant was diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. Depending the clarified extract was loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column was washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein was eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein were pooled and stored at 4°C. Protein concentration was estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins were refolded by diluting sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes were chosen so that the final protein concentration was between 50 to 100 micrograms/ml. The refolding solution was stirred gently at 4°C for 12-36 hours. The refolding reaction was quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution was filtered through a 0.22 micron filter and acetonitrile was added to 2-10% final concentration. The refolded protein was chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A₂₈₀ absorbance were analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein were pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO proteins were pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins were formulated into 20 mM Hepes, pH 6.8 with

0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides described herein were successfully expressed as described above.

EXAMPLE 101: Expression of PRO Polypeptides in Mammalian Cells

5 This example illustrates preparation of a glycosylated form of a desired PRO polypeptide by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO polypeptide-encoding DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO polypeptide DNA using ligation methods such as described in Sambrook et al., supra. The
10 resulting vector is called pRK5-PRO polypeptide.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μ g pRK5-PRO polypeptide DNA is mixed with about 1 μ g DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500
15 μ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 μ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

20 Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μ Ci/ml ³⁵S-cysteine and 200 μ Ci/ml ³⁵S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in
25 serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO polypeptide may be introduced into 293 cells transiently using the dextran sulfate method described by Sompanyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO polypeptide DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate
30 is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO polypeptide can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

35 In another embodiment, PRO polypeptides can be expressed in CHO cells. The pRK5-PRO polypeptide can be transfected into CHO cells using known reagents such as CaPO₄ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing

a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO polypeptide can then be concentrated and purified by any selected method.

Epitope-tagged PRO polypeptide may also be expressed in host CHO cells. The PRO polypeptide may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO polypeptide insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO polypeptide can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

Stable expression in CHO cells was performed using the following procedure. The proteins were expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins were fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs were subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., *Nucl. Acids Res.* 24: 9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA were introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect* (Quiagen), Dosper* or Fugene* (Boehringer Mannheim). The cells were grown and described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA were thawed by placement into water bath and mixed by vortexing. The contents were pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant was aspirated and the cells were resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells were then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells were transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, a 250 mL, 500 mL and 2000 mL spinners were seeded with 3×10^5 cells/mL. The cell media was exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in US Patent No. 5,122,469, issued June 16, 1992 was actually used. 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH were determined. On day 1, the spinner was sampled and sparging with filtered air was commenced. On day 2, the spinner was sampled,

the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion). Throughout the production, pH was adjusted as necessary to keep at around 7.2. After 10 days, or until viability dropped below 70%, the cell culture was harvested by centrifugation and filtering through a 0.22 µm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

5 For the poly-His tagged constructs, the proteins were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media was pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column was washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The
10 highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of were purified from the conditioned media as follows. The conditioned medium was pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer
15 before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 µL of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity was assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides described herein were successfully expressed as described above.

20

EXAMPLE 102: Expression of PRO Polypeptides in Yeast

The following method describes recombinant expression of a desired PRO polypeptide in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO polypeptides from the ADH2/GAPDH promoter. DNA encoding a desired PRO polypeptide, a selected signal
25 peptide and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of the PRO polypeptide. For secretion, DNA encoding the PRO polypeptide can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, the yeast alpha-factor secretory signal/leader sequence, and linker sequences (if needed) for expression of the PRO polypeptide.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described
30 above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO polypeptide can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge
35 filters. The concentrate containing the PRO polypeptide may further be purified using selected column chromatography resins.

Many of the PRO polypeptides described herein were successfully expressed as described above.

EXAMPLE 103: Expression of PRO Polypeptides in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO polypeptides in Baculovirus-infected insect cells.

The desired PRO polypeptide is fused upstream of an epitope tag contained with a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG).

5 A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the PRO polypeptide or the desired portion of the PRO polypeptide (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression
10 vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression is performed as described by O'Reilley et al.,
15 Baculovirus expression vectors: A laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO polypeptide can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% Glycerol; 0.1 % NP-40; 0.4 M KCl), and sonicated
20 twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% Glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at
25 which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% Glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO
30 polypeptide are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO polypeptide can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

PRO195, PRO526, PRO540, PRO846, PRO362, PRO363, PRO700, PRO707, PRO322, PRO719, PRO1083, PRO868, PRO866, PRO768, PRO788, PRO938, PRO827 and PRO1031 were successfully expressed
35 in baculovirus infected Sf9 insect cells. While the expression was actually performed in a 0.5-2 L scale, it can be readily scaled up for larger (e.g. 8 L) preparations. The proteins were expressed as an IgG construct (immunoadhesin), in which the protein extracellular region was fused to an IgG1 constant region sequence

containing the hinge, CH2 and CH3 domains and/or in poly-His tagged forms.

For expression in baculovirus infected Sf9 cells, following PCR amplification, the respective coding sequences were subcloned into a baculovirus expression vector (pb.PH.IgG for IgG fusions and pb.PH.His.c for poly-His tagged proteins), and the vector and Baculogold® baculovirus DNA (Pharmingen) were co-transfected into 105 *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711), using Lipofectin (Gibco BRL).
5 pb.PH.IgG and pb.PH.His are modifications of the commercially available baculovirus expression vector pVL1393 (Pharmingen), with modified polylinker regions to include the His or Fc tag sequences. The cells were grown in Hink's TNM-FH medium supplemented with 10% FBS (Hyclone). Cells were incubated for 5 days at 28°C. The supernatant was harvested and subsequently used for the first viral amplification by infecting Sf9
10 cells in Hink's TNM-FH medium supplemented with 10% FBS at an approximate multiplicity of infection (MOI) of 10. Cells were incubated for 3 days at 28°C. The supernatant was harvested and the expression of the constructs in the baculovirus expression vector was determined by batch binding of 1 ml of supernatant to 25 mL of Ni-NTA beads (QIAGEN) for histidine tagged proteins or Protein-A Sepharose CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.

15 The first viral amplification supernatant was used to infect a spinner culture (500 ml) of Sf9 cells grown in ESF-921 medium (Expression Systems LLC) at an approximate MOI of 0.1. Cells were incubated for 3 days at 28°C. The supernatant was harvested and filtered. Batch binding and SDS-PAGE analysis was repeated, as necessary, until expression of the spinner culture was confirmed.

The conditioned medium from the transfected cells (0.5 to 3 L) was harvested by centrifugation to
20 remove the cells and filtered through 0.22 micron filters. For the poly-His tagged constructs, the protein construct were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media were pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column was washed with additional equilibration buffer and the
25 protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of proteins were purified from the conditioned media as follows. The conditioned media were pumped onto a 5 ml Protein A column (Pharmacia) which had been
30 equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 mL of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity of the proteins was verified by SDS polyacrylamide gel (PAGE) electrophoresis and
35 N-terminal amino acid sequencing by Edman degradation.

PRO181, PRO195, PRO200, PRO320, PRO237, PRO273, PRO285, PRO337, PRO526, PRO540, PRO846, PRO362, PRO363, PRO617, PRO322, PRO1083, PRO868, 768, PRO792, PRO788, PRO162,

PRO1114, PRO827, PRO1075 and PRO1031 were successfully expressed in baculovirus infected Hi5 insect cells. While the expression was actually performed in a 0.5-2 L scale, it can be readily scaled up for larger (e.g. 8 L) preparations.

For expression in baculovirus-infected Hi5 insect cells, the PRO polypeptide-encoding DNA may be amplified with suitable systems, such as Pfu (Stratagene), or fused upstream (5'-of) of an epitope tag contained with a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the PRO polypeptide or the desired portion of the PRO polypeptide (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector. For example, derivatives of pVL1393 can include the Fc region of human IgG (pb.PH.IgG) or an 8 histidine (pb.PH.His) tag downstream (3'-of) the NAME sequence. Preferably, the vector construct is sequenced for confirmation.

Hi5 cells are grown to a confluency of 50% under the conditions of, 27°C, no CO₂, NO pen/strep. For each 150 mm plate, 30 ug of pIE based vector containing PRO polypeptide is mixed with 1 ml Ex-Cell medium (Media: Ex-Cell 401 + 1/100 L-Glu JRH Biosciences #14401-78P (note: this media is light sensitive)), and in a separate tube, 100 ul of CellFectin (CellFECTIN (GibcoBRL #10362-010) (vortexed to mix)) is mixed with 1 ml of Ex-Cell medium. The two solutions are combined and allowed to incubate at room temperature for 15 minutes. 8 ml of Ex-Cell media is added to the 2ml of DNA/CellFECTIN mix and this is layered on Hi5 cells that have been washed once with Ex-Cell media. The plate is then incubated in darkness for 1 hour at room temperature. The DNA/CellFECTIN mix is then aspirated, and the cells are washed once with Ex-Cell to remove excess CellFECTIN. 30 ml of fresh Ex-Cell media is added and the cells are incubated for 3 days at 28°C. The supernatant is harvested and the expression of the PRO polypeptide in the baculovirus expression vector can be determined by batch binding of 1 ml of supernatant to 25 mL of Ni-NTA beads (QIAGEN) for histidine tagged proteins or Protein-A Sepharose CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.

The conditioned media from the transfected cells (0.5 to 3 L) is harvested by centrifugation to remove the cells and filtered through 0.22 micron filters. For the poly-His tagged constructs, the protein comprising the PRO polypeptide is purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of proteins are purified from the conditioned media as follows. The conditioned media is pumped onto a 5 ml Protein A column (Pharmacia) which had been

equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 mL of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity of PRO polypeptide can be assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation and other analytical procedures as desired or necessary.

Many of the PRO polypeptides described herein were successfully expressed as described above.

EXAMPLE 104: Preparation of Antibodies that Bind to PRO Polypeptides

This example illustrates preparation of monoclonal antibodies which can specifically bind to a PRO polypeptide.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified PRO polypeptide, fusion proteins containing the PRO polypeptide, and cells expressing recombinant PRO polypeptide on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO polypeptide immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO polypeptide antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO polypeptide. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against the PRO polypeptide. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against the PRO polypeptide is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO polypeptide monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 105: Chimeric PRO Polypeptides

PRO polypeptides may be expressed as chimeric proteins with one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGSTM extension/affinity purification system (Immunex Corp., Seattle Wash.). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase (Invitrogen, San Diego Calif.) between the purification domain and the PRO polypeptide sequence may be useful to facilitate expression of DNA encoding the PRO polypeptide.

10 EXAMPLE 106: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSETM (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 107: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located

intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex
5 formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment
10 and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable
15 binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening
20 techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any
25 peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 108: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or
30 inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically,
35 by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins.

In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, *Biochemistry*, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, *J. Biochem.*, 113:742-746 (1993).

5 It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then
10 be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques
15 in place of or in addition to x-ray crystallography.

EXAMPLE 109: Ability of PRO Polypeptides to Inhibit Vascular Endothelial Growth Factor (VEGF) Stimulated Proliferation of Endothelial Cell Growth (Assay 9)

The ability of various PRO polypeptides to inhibit VEGF stimulated proliferation of endothelial cells
20 was tested. Polypeptides testing positive in this assay are useful for inhibiting endothelial cell growth in mammals where such an effect would be beneficial, e.g., for inhibiting tumor growth.

Specifically, bovine adrenal cortical capillary endothelial cells (ACE) (from primary culture, maximum of 12-14 passages) were plated in 96-well plates at 500 cells/well per 100 microliter. Assay media included low glucose DMEM, 10% calf serum, 2 mM glutamine, and 1X penicillin/streptomycin/fungizone. Control wells
25 included the following: (1) no ACE cells added; (2) ACE cells alone; (3) ACE cells plus 5 ng/ml FGF; (4) ACE cells plus 3 ng/ml VEGF; (5) ACE cells plus 3 ng/ml VEGF plus 1 ng/ml TGF-beta; and (6) ACE cells plus 3 ng/ml VEGF plus 5 ng/ml LIF. The test samples, poly-his tagged PRO polypeptides (in 100 microliter volumes), were then added to the wells (at dilutions of 1%, 0.1% and 0.01%, respectively). The cell cultures were incubated for 6-7 days at 37°C/5% CO₂. After the incubation, the media in the wells was aspirated, and
30 the cells were washed 1X with PBS. An acid phosphatase reaction mixture (100 microliter; 0.1M sodium acetate, pH 5.5, 0.1% Triton X-100, 10 mM p-nitrophenyl phosphate) was then added to each well. After a 2 hour incubation at 37°C, the reaction was stopped by addition of 10 microliters 1N NaOH. Optical density (OD) was measured on a microplate reader at 405 nm.

The activity of PRO polypeptides was calculated as the percent inhibition of VEGF (3 ng/ml) stimulated
35 proliferation (as determined by measuring acid phosphatase activity at OD 405 nm) relative to the cells without stimulation. TGF-beta was employed as an activity reference at 1 ng/ml, since TGF-beta blocks 70-90% of VEGF-stimulated ACE cell proliferation. The results are indicative of the utility of the PRO polypeptides in

cancer therapy and specifically in inhibiting tumor angiogenesis. Numerical values (relative inhibition) are determined by calculating the percent inhibition of VEGF stimulated proliferation by the PRO polypeptides relative to cells without stimulation and then dividing that percentage into the percent inhibition obtained by TGF- β at 1 ng/ml which is known to block 70-90% of VEGF stimulated cell proliferation. The results are considered positive if the PRO polypeptide exhibits 30% or greater inhibition of VEGF stimulation of endothelial cell growth (relative inhibition 30% or greater).

The following polypeptides tested positive in this assay: PRO200, PRO322 and PRO320.

EXAMPLE 110: Retinal Neuron Survival (Assay 52)

This example demonstrates that certain PRO polypeptides have efficacy in enhancing the survival of retinal neuron cells and, therefore, are useful for the therapeutic treatment of retinal disorders or injuries including, for example, treating sight loss in mammals due to retinitis pigmentosum, AMD, etc.

Sprague Dawley rat pups at postnatal day 7 (mixed population: glia and retinal neuronal types) are killed by decapitation following CO₂ anesthesia and the eyes are removed under sterile conditions. The neural retina is dissected away from the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca²⁺, Mg²⁺-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well in 96 well plates in DMEM/F12 supplemented with N2 and with or without the specific test PRO polypeptide. Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5% CO₂. After 2-3 days in culture, cells are stained with calcein AM then fixed using 4% paraformaldehyde and stained with DAPI for determination of total cell count. The total cells (fluorescent) are quantified at 20X objective magnification using CCD camera and NIH image software for MacIntosh. Fields in the well are chosen at random.

The effect of various concentration of PRO polypeptides are reported herein where percent survival is calculated by dividing the total number of calcein AM positive cells at 2-3 days in culture by the total number of DAPI-labeled cells at 2-3 days in culture. Anything above 30% survival is considered positive.

The following PRO polypeptides tested positive in this assay using polypeptide concentrations within the range of 0.01% to 1.0% in the assay: PRO200, PRO322, PRO540, PRO846 and PRO617.

EXAMPLE 111: Rod Photoreceptor Survival (Assay 56)

This assay shows that certain polypeptides of the invention act to enhance the survival/proliferation of rod photoreceptor cells and, therefore, are useful for the therapeutic treatment of retinal disorders or injuries including, for example, treating sight loss in mammals due to retinitis pigmentosum, AMD, etc. Sprague Dawley rat pups at 7 day postnatal (mixed population: glia and retinal neuronal cell types) are killed by decapitation following CO₂ anesthesia and the eyes are removed under sterile conditions. The neural retina is dissected away from the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca²⁺, Mg²⁺-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well

in 96 well plates in DMEM/F12 supplemented with N_2 . Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5% CO_2 . After 2-3 days in culture, cells are fixed using 4% paraformaldehyde, and then stained using CellTracker Green CMFDA. Rho 4D2 (ascites or IgG 1:100), a monoclonal antibody directed towards the visual pigment rhodopsin is used to detect rod photoreceptor cells by indirect immunofluorescence. The results are calculated as % survival: total number of calcein - rhodopsin positive cells at 2-3 days in culture, divided by the total number of rhodopsin positive cells at time 2-3 days in culture. The total cells (fluorescent) are quantified at 20x objective magnification using a CCD camera and NIH image software for MacIntosh. Fields in the well are chosen at random.

The following polypeptides tested positive in this assay: PRO200, PRO322, PRO540, PRO846 and PRO617.

EXAMPLE 112: Ability of PRO Polypeptides to Stimulate the Release of Proteoglycans from Cartilage (Assay 97)

The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

The metacarpophalangeal joint of 4-6 month old pigs was aseptically dissected, and articular cartilage was removed by free hand slicing being careful to avoid the underlying bone. The cartilage was minced and cultured in bulk for 24 hours in a humidified atmosphere of 95% air, 5% CO_2 in serum free (SF) media (DME/F12 1:1) with 0.1% BSA and 100U/ml penicillin and 100µg/ml streptomycin. After washing three times, approximately 100 mg of articular cartilage was aliquoted into micronics tubes and incubated for an additional 24 hours in the above SF media. PRO polypeptides were then added at 1% either alone or in combination with 18 ng/ml interleukin-1 α , a known stimulator of proteoglycan release from cartilage tissue. The supernatant was then harvested and assayed for the amount of proteoglycans using the 1,9-dimethyl-methylene blue (DMB) colorimetric assay (Farndale and Buttle, *Biochem. Biophys. Acta* 883:173-177 (1985)). A positive result in this assay indicates that the test polypeptide will find use, for example, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis.

When various PRO polypeptides were tested in the above assay, the polypeptides demonstrated a marked ability to stimulate release of proteoglycans from cartilage tissue both basally and after stimulation with interleukin-1 α and at 24 and 72 hours after treatment, thereby indicating that these PRO polypeptides are useful for stimulating proteoglycan release from cartilage tissue. As such, these PRO polypeptides are useful for the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. The polypeptides testing positive in this assay are: PRO200.

EXAMPLE 113: In Vitro Antiproliferative Assay (Assay 161)

The antiproliferative activity of various PRO polypeptides was determined in the investigational, disease-oriented *in vitro* anti-cancer drug discovery assay of the National Cancer Institute (NCI), using a sulforhodamine B (SRB) dye binding assay essentially as described by Skehan et al., *J. Natl. Cancer Inst.* 82:1107-1112 (1990). The 60 tumor cell lines employed in this study ("the NCI panel"), as well as conditions for their maintenance

and culture *in vitro* have been described by Monks et al., J. Natl. Cancer Inst. 83:757-766 (1991). The purpose of this screen is to initially evaluate the cytotoxic and/or cytostatic activity of the test compounds against different types of tumors (Monks et al., *supra*; Boyd, Cancer: Princ. Pract. Oncol. Update 3(10):1-12 [1989]).

Cells from approximately 60 human tumor cell lines were harvested with trypsin/EDTA (Gibco), washed once, resuspended in IMEM and their viability was determined. The cell suspensions were added by
5 pipet (100 μ L volume) into separate 96-well microtiter plates. The cell density for the 6-day incubation was less than for the 2-day incubation to prevent overgrowth. Inoculates were allowed a preincubation period of 24 hours at 37°C for stabilization. Dilutions at twice the intended test concentration were added at time zero in 100 μ L aliquots to the microtiter plate wells (1:2 dilution). Test compounds were evaluated at five half-log dilutions (1000 to 100,000-fold). Incubations took place for two days and six days in a 5% CO₂ atmosphere and 100%
10 humidity.

After incubation, the medium was removed and the cells were fixed in 0.1 ml of 10% trichloroacetic acid at 40°C. The plates were rinsed five times with deionized water, dried, stained for 30 minutes with 0.1 ml of 0.4% sulforhodamine B dye (Sigma) dissolved in 1% acetic acid, rinsed four times with 1% acetic acid to remove unbound dye, dried, and the stain was extracted for five minutes with 0.1 ml of 10 mM Tris base
15 [tris(hydroxymethyl)aminomethane], pH 10.5. The absorbance (OD) of sulforhodamine B at 492 nm was measured using a computer-interfaced, 96-well microtiter plate reader.

A test sample is considered positive if it shows at least 50% growth inhibitory effect at one or more concentrations. PRO polypeptides testing positive in this assay are shown in Table 7, where the abbreviations are as follows:

20 NSCL = non-small cell lung carcinoma
CNS = central nervous system

Table 7

	<u>Test compound</u>	<u>Tumor Cell Line Type</u>	<u>Cell Line Designation</u>
	PRO181	Leukemia	RPMI-8226
	PRO181	NSCL	NCI-H226; NCI-H522
	PRO181	Melanoma	MALME-3M; SK-MEL-5
5	PRO181	Ovarian	OVCAR-4
	PRO181	Breast	NCI/ADR-RES
	PRO181	Leukemia	MOLT-4
	PRO181	NSCL	NCI-H226*
	PRO181	CNS	SNB-19
10	PRO181	Ovarian	OVCAR-3; OVCAR-8
	PRO181	Renal	A498
	PRO181	Breast	MDA-MB-231/ATCC; MDA-N
	PRO181	Melanoma	LOX IMVI
	PRO181	Leukemia	CCRF-CEM; RPMI-8226*
15	PRO181	NSCL	HOP-62
	PRO181	Leukemia	HL-60 (TB)
	PRO237	Leukemia	K-562
	PRO237	NSCL	NCI-H322M
	PRO237	Colon	HCC-2998; HCT-15
20	PRO237	Colon	KM12
	PRO237	Prostate	DU-145
	PRO237	Breast	MDA-N
	PRO526	NSCL	HOP-62; NCI-H322M
	PRO526	Colon	HCT-116
25	PRO526	Melanoma	LOX IMVI; SK-MEL-2
	PRO526	Ovarian	OVCAR-3
	PRO526	Prostate	PC-3
	PRO526	NSCL	NCI-H226
	PRO526	CNS	SF-539
30	PRO526	Renal	CAKI-1; RXF 393
	PRO362	NSCL	NCI-H322M
	PRO362	Colon	HCT-116
	PRO362	CNS	SF-295
	PRO362	Melanoma	LOX IMVI
35	PRO362	Leukemia	MOLT-4; RPMI-8226; SR
	PRO362	Colon	COLO 205
	PRO362	Breast	HS 578T; MDA-N
	PRO362	Prostate	PC-3
	PRO362	Leukemia	HL-60 (TB); K-562
40	PRO362	NSCL	EKVX; NCI-H23
	PRO362	Colon	HCC-2998
	PRO362	CNS	U251
	PRO362	Melanoma	UACC-257; UACC-62
	PRO362	Ovarian	OVCAR-8
45	PRO362	Breast	T-47D
	PRO362	NSCL	NCI-H522
	PRO362	Renal	RXF 393; UO-31
	PRO362	Breast	MDA-MB-435
	PRO362	NSCL	HOP-62; NCI-H522
50	PRO362	Colon	KM12
	PRO362	Melanoma	MALME-3M; SK-MEL-2
	PRO362	Melanoma	SK-MEL-28; SK-MEL-5
	PRO362	Ovarian	OVCAR-3; OVCAR-4
	PRO362	Breast	MCF7
55	PRO866	Leukemia	HL-60 (TB); MOLT-4; SR

Table 7 (Continued)

	<u>Test compound</u>	<u>Tumor Cell Line Type</u>	<u>Cell Line Designation</u>
	PRO866	NSCL	HOP-62
	PRO866	NSCL	HOP-92
	PRO866	Colon	KM12
5	PRO866	CNS	SF-295
	PRO866	Ovarian	IGROV1
	PRO866	Breast	MDA-MB-435
	PRO866	Melanoma	LOX IMVI
	PRO320	Leukemia	CCRF-CEM; RPMI-8226
10	PRO320	NSCL	HOP62; NCI H322M
	PRO320	Colon	HCT-116
	PRO320	Renal	SN12C
	PRO320	Breast	MDA-N
	PRO320	Ovarian	OVCAR-3
15	PRO320	Melanoma	MALME-3M

* cytotoxic

The results of these assays demonstrate that the positive testing PRO polypeptides are useful for inhibiting neoplastic growth in a number of different tumor cell types and may be used therapeutically therefor.

- 20 Antibodies against these PRO polypeptides are useful for affinity purification of these useful polypeptides. Nucleic acids encoding these PRO polypeptides are useful for the recombinant preparation of these polypeptides.

EXAMPLE 114: Gene Amplification in Tumors

- 25 This example shows that certain PRO polypeptide-encoding genes are amplified in the genome of certain human lung, colon and/or breast cancers and/or cell lines. Amplification is associated with overexpression of the gene product, indicating that the polypeptides are useful targets for therapeutic intervention in certain cancers such as colon, lung, breast and other cancers and diagnostic determination of the presence of those cancers. Therapeutic agents may take the form of antagonists of the PRO polypeptide, for example, murine-human chimeric, humanized or human antibodies against a PRO polypeptide.

- 30 The starting material for the screen was genomic DNA isolated from a variety cancers. The DNA is quantitated precisely, *e.g.*, fluorometrically. As a negative control, DNA was isolated from the cells of ten normal healthy individuals which was pooled and used as assay controls for the gene copy in healthy individuals (not shown). The 5' nuclease assay (for example, TaqMan™) and real-time quantitative PCR (for example, ABI Prizm 7700 Sequence Detection System™ (Perkin Elmer, Applied Biosystems Division, Foster City, CA)), were
35 used to find genes potentially amplified in certain cancers. The results were used to determine whether the DNA encoding the PRO polypeptide is over-represented in any of the primary lung or colon cancers or cancer cell lines or breast cancer cell lines that were screened. The primary lung cancers were obtained from individuals with tumors of the type and stage as indicated in Table 8. An explanation of the abbreviations used for the designation of the primary tumors listed in Table 8 and the primary tumors and cell lines referred to throughout
40 this example are given below.

The results of the TaqMan™ are reported in delta (Δ) Ct units. One unit corresponds to 1 PCR cycle or approximately a 2-fold amplification relative to normal, two units corresponds to 4-fold, 3 units to 8-fold amplification and so on. Quantitation was obtained using primers and a TaqMan™ fluorescent probe derived

from the PRO polypeptide-encoding gene. Regions of the PRO polypeptide-encoding gene which are most likely to contain unique nucleic acid sequences and which are least likely to have spliced out introns are preferred for the primer and probe derivation, e.g., 3'-untranslated regions. The sequences for the primers and probes (forward, reverse and probe) used for the PRO polypeptide gene amplification analysis were as follows:

PRO853 (DNA48227-1350)

- 5 48227.tm.fl
5'-GGCACTTCATGGTCCTTGAAA-3' (SEQ ID NO:539)
48227.tm.pl
5'-CGGATGTGTGTGAGGCCATGCC-3' (SEQ ID NO:540)
48227.tm.r1
10 5'-GAAAGTAACCACGGAGGTCAAGAT-3' (SEQ ID NO:541)

PRO1017 (DNA56112-1379):

- 56112.tm.fl
5'-CCTCCTCCGAGACTGAAAGCT-3' (SEQ ID NO:542)
15 56112.tm.pl
5'-TCGCGTTGCTTTTTCTCGCGTG-3' (SEQ ID NO:543)
56112.tm.r1
5'-GCGTGCGTCAGGTCCA-3' (SEQ ID NO:544)

20 PRO213-1 (DNA30943-1163-1):

- 30943.tm.f3:
5'-CGTTCGTGCAGCGTGTGTA-3' (SEQ ID NO:545)
30943.tm.p3:
5'-CTTCCTCACCACTGCGACGGG-3' (SEQ ID NO:546)
25 30943.tm.r3:
5'-GGTAGGCGGTCCTATAGATGGTT-3' (SEQ ID NO:547)
30943.tm.fl:
5'-AGATGTGGATGAATGCAGTGCTA-3' (SEQ ID NO:548)
30943.tm.pl:
30 5'-ATCAACACCGCCGGCAGTTACTGG-3' (SEQ ID NO:549)
30943.tm.r1:
5'-ACAGAGTGTACCGTCTGCAGACA-3' (SEQ ID NO:550)
30943.3trn-5:
5'-AGCCTCCTGGTGCACTCCT-3' (SEQ ID NO:551)
35 30943.3trn-probe:
5'-CGACTCCCTGAGCGAGCAGATTTC-3' (SEQ ID NO:552)

- 30943.3tm-3:
5'-GCTGGGCAGTCACGAGTCTT-3' (SEQ ID NO:553)
- PRO237 (DNA34353-1428):
34353.tm.f:
5 5'-AATCCTCCATCTCAGATCTTCCAG-3' (SEQ ID NO:554)
34353.tm.p:
5'-CCTCAGCGGTAACAGCCGGCC-3' (SEQ ID NO:555)
34353.tm.r:
5'-TGGGCCAAGGGCTGC-3' (SEQ ID NO:556)
- 10 PRO324 (DNA36343-1310):
36343.tmf1:
5'-TGGTGGATAACCAACAAGATGG-3' (SEQ ID NO:557)
36343.tmp1:
15 5'-GAGTCTGCATCCACACCACTCTTAAAGTTCTCAA-3' (SEQ ID NO:558)
36343.tmr1:
5'-CAGGTGCTCTTTTCAGTCATGTTT-3' (SEQ ID NO:559)
- PRO351 (DNA40571-1315):
20 40571.tm.fl:
5'-TGGCCATTCTCAGGACAAGAG-3' (SEQ ID NO:560)
40571.tm.pl:
5'-CAGTAATGCCATTTGCCTGCCTGCAT-3' (SEQ ID NO:561)
40571.tm.rl:
25 5'-TGCCTGGAATCACATGACA-3' (SEQ ID NO:562)
- PRO362 (DNA45416-1251):
45416.tm.fl:
5'-TGTGGCACAGACCCAATCCT-3' (SEQ ID NO:563)
30 45416.tm.pl:
5'-GACCCTGAAGGCCTCCGGCCT-3' (SEQ ID NO:564)
45416.tm.rl:
5'-GAGAGAGGGAAGGCAGCTATGTC-3' (SEQ ID NO:565)
- 35 PRO615 (DNA48304-1323):
48304.tm.fl:
5'-CAGCCCCTCTCTTTCACCTGT-3' (SEQ ID NO:566)

- 48304.tm.p1:
5'-CCATCCTGTGCAGCTGACACACAGC-3' (SEQ ID NO:567)
48304.tm.r1:
5'-GC CAGGCTATGA GGCTCCTT-3' (SEQ ID NO:568)
- 5 PRO531 (DNA48314-1320):
48314.tm.f1:
5'-TTCAAGTTCCTGAAGCCGATTAT-3' (SEQ ID NO:569)
48814.tm.p1:
5'-CCAACTTCCCTCCCCAGTGCCCT-3' (SEQ ID NO:570)
10 48814.tm.r1:
5'-TTGGGGAAGGTAGAAATTCCTTGAT-3' (SEQ ID NO:571)
- PRO618 (DNA49152-1324):
49152.tm.f1:
15 5'-CCCTTCTGCCTCCCAATTCT-3' (SEQ ID NO:572)
49152.tm.p1:
5'-TCTCCTCCGTCCCCCTCCTCCACT-3' (SEQ ID NO:573)
49152.tm.r1:
5'-TGAGCCACTGCCTTGCAATTA-3' (SEQ ID NO:574)
20
- PRO772 (DNA49645-1347):
49645.tm.f2:
5'-TCTGCAGACGCGATGGATAA-3' (SEQ ID NO:575)
49645.tm.p2:
25 5'-CCGAAAATAAAACATCGCCCCTTCTGC-3' (SEQ ID NO:576)
49645.tm.r2:
5'-CACGTGGCCTTTCACACTGA-3' (SEQ ID NO:577)
49645.tm.f1:
5'-ACTTGTGACAGCAGTATGCTGTCTT-3' (SEQ ID NO:578)
30 49645.tm.p1:
5'-AAGCTTCTGTTCAATCCCAGCGGTCC-3' (SEQ ID NO:579)
49645.tm.r1:
5'-ATGCACAGGCTTTTTCTGGTAA-3' (SEQ ID NO:580)
- 35 PRO703 (DNA50913-1287):
50913.tm.f1:
5'-GCAGGAAACCTTCGAATCTGAG-3' (SEQ ID NO:581)

50913.tm.p1:

5'-ACACCTGAGGCACCTGAGAGAGGAACTCT-3' (SEQ ID NO:582)

50913.tm.r1:

5'-GACAGCCCAGTACACCTGCAA-3' (SEQ ID NO:583)

5 PRO792 (DNA56352-1358):

56352.tm.fl:

5'-GACGGCTGGATCTGTGAGAAA-3' (SEQ ID NO:584)

56352.tm.p1:

5'-CACAAGTGTGACCCCGCCCA-3' (SEQ ID NO:585)

10 56352.tm.r1:

5'-CCAGGATACGACATGCTGCAA-3' (SEQ ID NO:586)

PRO474 (DNA56045-1380):

56045.tm.fl:

15 5'-AAACTCCAACCTGTATCAGATGCA-3' (SEQ ID NO:587)

56045.tm.p1:

5'-CCCCCAAGCCCTTAGACTCTAAGCCC-3' (SEQ ID NO:588)

56045.tm.r1:

5'-GACCCGGCACCTTGCTAAC-3' (SEQ ID NO:589)

20

PRO274 (DNA39987-1184):

39987.tm.f:

5'-GGACGGTCAGTCAGGATGACA-3' (SEQ ID NO:590)

39987.tm.p:

25 5'-TTCGGCATCATCTCTTCCCTCTCCC-3' (SEQ ID NO:591)

39987.tm.r:

5'-ACAAAAAAAAGGGAACAAAATACGA-3' (SEQ ID NO:592)

PRO381 (DNA44194-1317)

30 44194.tm.f :

5'-CTTTGAATAGAAGACTTCTGGACAATTT-3' (SEQ ID NO:593)

44194.tm.p:

5'-TTGCAACTGGGAATATACCACGACATGAGA-3' (SEQ ID NO:594)

44194.tm.r:

35 5'-TAGGGTGCTAATTTGTGCTATAACCT-3' (SEQ ID NO:595)

44194.tm.f2:

5'-GGCTCTGAGTCTCTGCTTGA-3' (SEQ ID NO:596)

44194.tm.p2:

5'-TCCAACAACCATTTTCCTCTGGTCC-3' (SEQ ID NO:597)

44194.tm.r2:

5'-AAGCAGTAGCCATTAACAAGTCA-3' (SEQ ID NO:598)

5 PRO717 (DNA50988-1326):

50988.tm.f3:

5'-CAAGCGTCCAGGTTTATTGA-3' (SEQ ID NO:599)

50988.tm.r3:

5'-GACTACAAGGCGCTCAGCTA-3' (SEQ ID NO:600)

10 50988.tm.p3:

5'-CCGGCTGGGTCTCACTCCTCC-3' (SEQ ID NO:601)

PRO1330 and PRO1449 (DNA64907-1163 and DNA64908-1163, respectively):

30943.tm.f3:

15 5'-CGTTCGTGCAGCGTGTGTA-3' (SEQ ID NO:602)

30943.tm.p3:

5'-CTTCCTCACCACTGCGACG GG-3' (SEQ ID NO:603)

30943.tm.r3:

5'-GGTAGGCGGTCCTATAGATGGTT-3' (SEQ ID NO:604)

20 30943.tm.f1:

5'-AGATG TGGATGAATG CAGTGCTA-3' (SEQ ID NO:605)

30943.tm.p1:

5'-ATCAACACCGCCGGCAGTTACTGG-3' (SEQ ID NO:606)

30943.tm.r1:

25 5'-ACAGAGTGTACCGTCTGCAGACA-3' (SEQ ID NO:607)

30943.3trn-5:

5'-AGCCTCCTGGTGCACTCCT-3' (SEQ ID NO:608)

30943.3trn-probe:

5'-CGACTCCCTGAGCGAGCAGATTTCC-3' (SEQ ID NO:609)

30 30943.3trn-3:

5'-GCTGGGCAGTCACGAGTCTT-3' (SEQ ID NO:610)

35 The 5' nuclease assay reaction is a fluorescent PCR-based technique which makes use of the 5' exonuclease activity of Taq DNA polymerase enzyme to monitor amplification in real time. Two oligonucleotide primers (forward [.f] and reverse [.r]) are used to generate an amplicon typical of a PCR reaction. A third oligonucleotide, or probe (.p), is designed to detect nucleotide sequence located between the two PCR primers. The probe is non-extendible by Taq DNA polymerase enzyme, and is labeled with a reporter fluorescent dye

and a quencher fluorescent dye. Any laser-induced emission from the reporter dye is quenched by the quenching dye when the two dyes are located close together as they are on the probe. During the amplification reaction, the Taq DNA polymerase enzyme cleaves the probe in a template-dependent manner. The resultant probe fragments disassociate in solution, and signal from the released reporter dye is free from the quenching effect of the second fluorophore. One molecule of reporter dye is liberated for each new molecule synthesized, and
5 detection of the unquenched reporter dye provides the basis for quantitative interpretation of the data.

The 5' nuclease procedure is run on a real-time quantitative PCR device such as the ABI Prism 7700TM Sequence Detection. The system consists of a thermocycler, laser, charge-coupled device (CCD) camera and computer. The system amplifies samples in a 96-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 96 wells, and detected
10 at the CCD. The system includes software for running the instrument and for analyzing the data.

5' Nuclease assay data are initially expressed as Ct, or the threshold cycle. This is defined as the cycle at which the reporter signal accumulates above the background level of fluorescence. The ΔCt values are used as quantitative measurement of the relative number of starting copies of a particular target sequence in a nucleic acid sample when comparing cancer DNA results to normal human DNA results.

15 Table 8 describes the stage, T stage and N stage of various primary tumors which were used to screen the PRO polypeptide compounds of the invention.

Table 8
Primary Lung and Colon Tumor Profiles

	<u>Primary Tumor Stage</u>	<u>Stage</u>	<u>Other Stage</u>	<u>Dukes Stage</u>	<u>T Stage</u>	<u>N Stage</u>
	Human lung tumor AdenoCa (SRCC724) [LT1]	IIA			T1	N1
5	Human lung tumor SqCCa (SRCC725) [LT1a]	IIB			T3	N0
	Human lung tumor AdenoCa (SRCC726) [LT2]	IB			T2	N0
	Human lung tumor AdenoCa (SRCC727) [LT3]	IIIA			T1	N2
	Human lung tumor AdenoCa (SRCC728) [LT4]	IB			T2	N0
	Human lung tumor SqCCa (SRCC729) [LT6]	IB			T2	N0
10	Human lung tumor Aden/SqCCa (SRCC730) [LT7]	IA			T1	N0
	Human lung tumor AdenoCa (SRCC731) [LT9]	IB			T2	N0
	Human lung tumor SqCCa (SRCC732) [LT10]	IIB			T2	N1
	Human lung tumor SqCCa (SRCC733) [LT11]	IIA			T1	N1
	Human lung tumor AdenoCa (SRCC734) [LT12]	IV			T2	N0
15	Human lung tumor AdenoSqCCa (SRCC735) [LT13]	IIB			T2	N0
	Human lung tumor SqCCa (SRCC736) [LT15]	IB			T2	N0
	Human lung tumor SqCCa (SRCC737) [LT16]	IB			T2	N0
	Human lung tumor SqCCa (SRCC738) [LT17]	IIB			T2	N1
	Human lung tumor SqCCa (SRCC739) [LT18]	IB			T2	N0
20	Human lung tumor SqCCa (SRCC740) [LT19]	IB			T2	N0
	Human lung tumor LCCa (SRCC741) [LT21]	IIB			T3	N1
	Human lung AdenoCa (SRCC811) [LT22]	IA			T1	N0
	Human colon AdenoCa (SRCC742) [CT2]		M1	D	pT4	N0
	Human colon AdenoCa (SRCC743) [CT3]			B	pT3	N0
25	Human colon AdenoCa (SRCC744) [CT8]			B	T3	N0
	Human colon AdenoCa (SRCC745) [CT10]			A	pT2	N0
	Human colon AdenoCa (SRCC746) [CT12]		MO, R1	B	T3	N0
	Human colon AdenoCa (SRCC747) [CT14]		pMO, RO	B	pT3	pN0
	Human colon AdenoCa (SRCC748) [CT15]		M1, R2	D	T4	N2
30	Human colon AdenoCa (SRCC749) [CT16]		pMO	B	pT3	pN0
	Human colon AdenoCa (SRCC750) [CT17]			C1	pT3	pN1
	Human colon AdenoCa (SRCC751) [CT1]		MO, R1	B	pT3	N0
	Human colon AdenoCa (SRCC752) [CT4]			B	pT3	M0
	Human colon AdenoCa (SRCC753) [CT5]		G2	C1	pT3	pN0
35	Human colon AdenoCa (SRCC754) [CT6]		pMO, RO	B	pT3	pN0
	Human colon AdenoCa (SRCC755) [CT7]		G1	A	pT2	pN0
	Human colon AdenoCa (SRCC756) [CT9]		G3	D	pT4	pN2
	Human colon AdenoCa (SRCC757) [CT11]			B	T3	N0
40	Human colon AdenoCa (SRCC758) [CT18]		MO, RO	B	pT3	pN0

DNA Preparation:

DNA was prepared from cultured cell lines, primary tumors, normal human blood. The isolation was performed using purification kit, buffer set and protease and all from Quiagen, according to the manufacturer's instructions and the description below.

45 Cell culture lysis:

Cells were washed and trypsinized at a concentration of 7.5×10^8 per tip and pelleted by centrifuging at 1000 rpm for 5 minutes at 4°C, followed by washing again with 1/2 volume of PBS recentrifugation. The pellets were washed a third time, the suspended cells collected and washed 2x with PBS. The cells were then suspended into 10 ml PBS. Buffer C1 was equilibrated at 4°C. Qiagen protease #19155 was diluted into 6.25 ml cold ddH₂O to a final concentration of 20 mg/ml and equilibrated at 4°C. 10 ml of G2 Buffer was prepared by diluting Qiagen RNase A stock (100 mg/ml) to a final concentration of 200 µg/ml.

Buffer C1 (10 ml, 4°C) and ddH₂O (40 ml, 4°C) were then added to the 10 ml of cell suspension, mixed by inverting and incubated on ice for 10 minutes. The cell nuclei were pelleted by centrifuging in a Beckman swinging bucket rotor at 2500 rpm at 4°C for 15 minutes. The supernatant was discarded and the nuclei were suspended with a vortex into 2 ml Buffer C1 (at 4°C) and 6 ml ddH₂O, followed by a second 4°C centrifugation at 2500 rpm for 15 minutes. The nuclei were then resuspended into the residual buffer using 200 μ l per tip.

5 G2 buffer (10 ml) was added to the suspended nuclei while gentle vortexing was applied. Upon completion of buffer addition, vigorous vortexing was applied for 30 seconds. Quiagen protease (200 μ l, prepared as indicated above) was added and incubated at 50°C for 60 minutes. The incubation and centrifugation was repeated until the lysates were clear (*e.g.*, incubating additional 30-60 minutes, pelleting at 3000 x g for 10 min., 4°C).

Solid human tumor sample preparation and lysis:

10 Tumor samples were weighed and placed into 50 ml conical tubes and held on ice. Processing was limited to no more than 250 mg tissue per preparation (1 tip/preparation). The protease solution was freshly prepared by diluting into 6.25 ml cold ddH₂O to a final concentration of 20 mg/ml and stored at 4°C. G2 buffer (20 ml) was prepared by diluting DNase A to a final concentration of 200 mg/ml (from 100 mg/ml stock). The tumor tissue was homogenated in 19 ml G2 buffer for 60 seconds using the large tip of the polytron in a laminar-

15 flow TC hood in order to avoid inhalation of aerosols, and held at room temperature. Between samples, the polytron was cleaned by spinning at 2 x 30 seconds each in 2L ddH₂O, followed by G2 buffer (50 ml). If tissue was still present on the generator tip, the apparatus was disassembled and cleaned.

Quiagen protease (prepared as indicated above, 1.0 ml) was added, followed by vortexing and incubation at 50°C for 3 hours. The incubation and centrifugation was repeated until the lysates were clear (*e.g.*,

20 incubating additional 30-60 minutes, pelleting at 3000 x g for 10 min., 4°C).

Human blood preparation and lysis:

Blood was drawn from healthy volunteers using standard infectious agent protocols and citrated into 10 ml samples per tip. Quiagen protease was freshly prepared by dilution into 6.25 ml cold ddH₂O to a final concentration of 20 mg/ml and stored at 4°C. G2 buffer was prepared by diluting RNase A to a final

25 concentration of 200 μ g/ml from 100 mg/ml stock. The blood (10 ml) was placed into a 50 ml conical tube and 10 ml C1 buffer and 30 ml ddH₂O (both previously equilibrated to 4°C) were added, and the components mixed by inverting and held on ice for 10 minutes. The nuclei were pelleted with a Beckman swinging bucket rotor at 2500 rpm, 4°C for 15 minutes and the supernatant discarded. With a vortex, the nuclei were suspended into 2 ml C1 buffer (4°C) and 6 ml ddH₂O (4°C). Vortexing was repeated until the pellet was white. The nuclei

30 were then suspended into the residual buffer using a 200 μ l tip. G2 buffer (10 ml) were added to the suspended nuclei while gently vortexing, followed by vigorous vortexing for 30 seconds. Quiagen protease was added (200 μ l) and incubated at 50°C for 60 minutes. The incubation and centrifugation was repeated until the lysates were clear (*e.g.*, incubating additional 30-60 minutes, pelleting at 3000 x g for 10 min., 4°C).

Purification of cleared lysates:

35 (1) Isolation of genomic DNA:

Genomic DNA was equilibrated (1 sample per maxi tip preparation) with 10 ml QBT buffer. QF elution buffer was equilibrated at 50°C. The samples were vortexed for 30 seconds, then loaded onto equilibrated tips

and drained by gravity. The tips were washed with 2 x 15 ml QC buffer. The DNA was eluted into 30 ml silanized, autoclaved 30 ml Corex tubes with 15 ml QF buffer (50°C). Isopropanol (10.5 ml) was added to each sample, the tubes covered with parafin and mixed by repeated inversion until the DNA precipitated. Samples were pelleted by centrifugation in the SS-34 rotor at 15,000 rpm for 10 minutes at 4°C. The pellet location was marked, the supernatant discarded, and 10 ml 70% ethanol (4°C) was added. Samples were pelleted again by centrifugation on the SS-34 rotor at 10,000 rpm for 10 minutes at 4°C. The pellet location was marked and the supernatant discarded. The tubes were then placed on their side in a drying rack and dried 10 minutes at 37°C, taking care not to overdry the samples.

After drying, the pellets were dissolved into 1.0 ml TE (pH 8.5) and placed at 50°C for 1-2 hours. Samples were held overnight at 4°C as dissolution continued. The DNA solution was then transferred to 1.5 ml tubes with a 26 gauge needle on a tuberculin syringe. The transfer was repeated 5x in order to shear the DNA. Samples were then placed at 50°C for 1-2 hours.

(2) Quantitation of genomic DNA and preparation for gene amplification assay:

The DNA levels in each tube were quantified by standard A_{260} , A_{280} spectrophotometry on a 1:20 dilution (5 μ l DNA + 95 μ l ddH₂O) using the 0.1 ml quartz cuvetts in the Beckman DU640 spectrophotometer. A_{260}/A_{280} ratios were in the range of 1.8-1.9. Each DNA samples was then diluted further to approximately 200 ng/ml in TE (pH 8.5). If the original material was highly concentrated (about 700 ng/ μ l), the material was placed at 50°C for several hours until resuspended.

Fluorometric DNA quantitation was then performed on the diluted material (20-600 ng/ml) using the manufacturer's guidelines as modified below. This was accomplished by allowing a Hoeffer DyNA Quant 200 fluorometer to warm-up for about 15 minutes. The Hoechst dye working solution (#H33258, 10 μ l, prepared within 12 hours of use) was diluted into 100 ml 1 x TNE buffer. A 2 ml cuvette was filled with the fluorometer solution, placed into the machine, and the machine was zeroed. pGEM 3Zf(+) (2 μ l, lot #360851026) was added to 2 ml of fluorometer solution and calibrated at 200 units. An additional 2 μ l of pGEM 3Zf(+) DNA was then tested and the reading confirmed at 400 +/- 10 units. Each sample was then read at least in triplicate. When 3 samples were found to be within 10% of each other, their average was taken and this value was used as the quantification value.

The fluorometrically determined concentration was then used to dilute each sample to 10 ng/ μ l in ddH₂O. This was done simultaneously on all template samples for a single TaqMan plate assay, and with enough material to run 500-1000 assays. The samples were tested in triplicate with Taqman™ primers and probe both B-actin and GAPDH on a single plate with normal human DNA and no-template controls. The diluted samples were used provided that the CT value of normal human DNA subtracted from test DNA was +/- 1 Ct. The diluted, lot-qualified genomic DNA was stored in 1.0 ml aliquots at -80°C. Aliquots which were subsequently to be used in the gene amplification assay were stored at 4°C. Each 1 ml aliquot is enough for 8-9 plates or 64 tests.

Gene amplification assay:

The PRO polypeptide compounds of the invention were screened in the following primary tumors and the resulting Δ Ct values greater than or equal to 1.0 are reported in Table 9 below.

Table 9
 ACt values in lung and colon primary tumor and cell line models

Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
LT-1	1.60	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.60
LT-1a	1.24	1.04	---	---	---	---	1.70	---	1.785	---	1.33	1.22	1.16	1.94	---	---	---	1.24
LT2	---	---	---	---	1.39	---	---	---	---	---	---	---	---	---	---	---	---	---
LT3	1.51	1.74	---	---	---	1.31 1.55 1.44	1.95 1.24	---	2.38	1.03	1.11	1.77	1.10	2.55 1.52	---	---	---	1.51
LT4	2.26	---	---	---	1.00	---	1.46	---	---	---	---	---	---	---	1.24	---	---	2.26
LT6	1.56	1.16	---	---	---	1.00	2.07	---	2.80	---	1.07	1.15	1.81	2.10 2.28	---	---	---	1.56
LT7	2.45	1.44	---	---	---	1.09 1.03	---	---	1.12	---	---	1.44	---	1.06	---	---	---	2.45
LT9	1.24	---	---	1.19	---	1.04 1.14	1.10	---	2.74	1.39 1.11	1.62	---	1.99	2.56 2.59	---	---	---	1.24
LT10	---	1.20	---	1.06	1.69	1.18 1.11	1.96 1.16	---	3.52	1.29 1.29	1.46	1.48	2.00	2.63 2.85	---	---	---	---
LT11	2.26 2.85 2.25 1.79	---	1.34	1.02	---	1.46 1.72 1.27 1.25 1.06	1.79	1.03	1.54 2.94 1.41	1.84	1.45	1.90 1.83	1.20	1.36 5.21	---	---	---	2.26 2.85 2.25 1.79

Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
LT12	1.86	---	1.92	---	---	2.08	1.86	1.18	1.77	---	---	1.38	---	1.64	---	---	---	1.86
	4.32	---	---	---	---	1.87	---	---	3.02	---	---	1.62	---	5.01	---	---	---	4.32
	2.59	---	---	---	---	1.41	---	---	1.82	---	---	---	---	---	---	---	---	2.59
	1.55	---	---	---	---	1.50	---	---	---	---	---	---	---	---	---	---	---	1.55
LT13	1.98	1.05	---	1.23	---	1.39	2.53	1.33	1.55	---	1.18	1.33	1.33	1.03	---	---	7.03	1.98
	2.52	---	---	---	---	1.09	2.06	---	2.14	---	---	1.20	---	1.00	---	---	---	2.52
	2.38	---	---	---	---	1.03	1.31	---	2.03	---	---	---	---	4.54	---	---	---	2.38
	---	---	---	---	---	---	---	---	---	---	---	---	---	1.14	---	---	---	---
LT15	1.40	---	---	1.14	---	1.67	2.56	1.28	2.23	---	1.47	1.45	1.04	1.35	---	---	2.71	1.40
	1.58	---	---	---	---	1.47	2.95	---	2.01	---	---	1.44	---	1.86	---	---	---	1.58
	2.69	---	---	---	---	1.09	1.31	---	2.50	---	---	---	---	4.97	---	---	---	2.69
	---	---	---	---	---	1.05	---	---	---	---	---	---	---	1.52	---	---	---	---
LT16	1.22	1.22	1.63	1.09	---	1.32	---	1.33	2.98	---	---	1.07	---	4.23	1.00	---	5.48	1.22
	2.77	---	---	---	---	1.38	---	---	1.77	---	---	---	---	1.52	---	---	---	2.77
	1.75	---	---	---	---	---	---	---	---	---	---	---	---	1.17	---	---	---	1.75
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
LT17	4.58	1.07	1.75	1.46	---	1.66	1.12	1.21	2.90	1.04	1.42	1.24	1.35	1.40	---	---	---	4.58
	3.73	---	---	---	---	1.59	1.53	---	1.62	---	---	1.61	1.115	5.45	---	---	---	3.73
	5.55	---	---	---	---	1.21	---	---	---	---	---	---	---	---	---	---	---	5.55
	---	---	---	---	---	1.50	---	---	---	---	---	---	---	---	---	---	---	---
LT18	---	---	---	1.07	---	---	---	---	3.28	---	---	---	---	5.31	1.61	---	---	---
	---	---	---	---	---	---	---	---	1.68	---	---	---	---	---	---	---	---	---

Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
LT19	1.03 1.22 1.26	---	1.90	1.33	---	1.59 1.50 1.03 1.48	2.08 2.95	---	2.54 2.98 1.21	---	1.60	1.38 1.19	1.62	1.59 1.84 4.84	---	---	---	1.03 1.22 1.26
LT21	1.86 1.83 3.21	---	1.15	1.27	---	1.19 1.09 1.06	---	---	3.14	---	---	1.22	---	5.15	---	---	---	1.86 1.83 3.21
LT22	1.61	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.61
CT2	1.61 2.11	---	---	---	---	1.36 1.25	2.21 2.55 1.90	2.4	3.72 2.55	---	---	2.10	1.46	2.67 1.65 1.48	---	---	---	1.61 2.11
CT3	---	---	---	---	---	1.12	1.50	1.52	3.91 1.58	---	---	1.62	---	2.41 1.02	---	---	---	---
CT8	2.80	---	---	---	---	---	1.15 1.34	1.55	2.66	---	---	1.06	---	2.34	---	---	---	2.80
CT10	2.39	---	---	---	---	1.55	1.75 1.47	1.97	3.57 1.78	---	---	1.96	---	2.23 1.21	---	---	---	2.39
CT12	3.45	---	---	---	---	1.08	1.93 1.30	1.36	3.50 1.08	---	---	1.57	---	2.46	---	---	---	3.45
CT14	3.79	---	---	---	---	1.76 1.02	1.47 1.11	1.75	3.88 1.86	---	---	1.19	---	2.83	---	---	---	3.79
CT15	3.66	---	---	---	---	1.23	2.44 1.33	1.75	3.62	---	---	1.70	---	2.89	---	---	2.61	3.66
CT16	2.66	---	---	---	---	1.29	1.95	1.11	3.12	---	---	1.51	---	2.60	---	---	2.21	2.66
CT17	3.63	---	---	---	---	1.44	2.19	1.11	3.34	---	---	1.31	---	2.33	---	---	3.31	3.63

Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
CT1	---	---	---	---	---	---	---	1.09	---	---	---	1.08	---	1.00	---	---	---	---
CT4	1.18	---	---	---	---	1.17	---	1.16	1.11	---	---	1.63	---	1.13	---	---	---	1.18
CT5	1.25	---	---	---	---	1.12	1.59	1.95	2.21	---	---	1.50	---	1.84	---	---	---	1.25
						1.16	1.35							2.05				
							2.11											
CT6	1.27	---	---	---	---	---	---	---	1.12	---	---	1.38	---	1.24	---	---	---	1.27
														1.36				
CT7	---	---	---	---	---	---	---	1.14	---	---	---	1.50	---	---	---	---	---	---
CT9	---	---	---	---	---	---	1.28	---	1.29	---	---	---	---	---	---	---	---	---
CT11	---	---	---	---	---	1.74	1.49	1.88	1.48	---	---	1.99	---	2.11	---	---	---	---
						1.17								2.13				
CT18	---	---	---	---	---	1.36	---	---	---	---	---	1.15	---	9.66	---	---	---	---
Calu-1	1.35	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.77	1.35
	2.95																	2.95
H441	2.00	---	---	---	---	---	---	1.71	---	---	---	---	---	---	---	---	2.57	2.00
H522	---	---	---	---	---	---	---	1.03	---	---	---	---	---	---	---	---	3.78	---
H810	2.76	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.84	2.76
HT29	1.31	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.71	1.31
SW403	2.08	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.09	2.08
LS174T	1.61	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.90	1.61
HCT15	1.22	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.46	1.22
HCC2998	1.73	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.20	1.73

Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
HF- 000643	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	4.83	---	---
HF- 000840	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.08	---	---
HF- 000811	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.09 3.15	---	---
HF- 001294	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.14 1.08	---	---
HF- 001296	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	3.18 3.53	---	---
HF- 001291	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.17	---	---
A549	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.66	---
H460	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.50	---
SKMES1	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.15	---
SW620	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.36	---
Colo320	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.99 2.73	---
HCT116	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.90	---
SKCO1	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	3.13	---
Colo205	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.48	---
KM12	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.67	---

Summary

Because amplification of the various DNA's as described above occurs in various tumors, it is likely associated with tumor formation and/or growth. As a result, antagonists (*e.g.*, antibodies) directed against these polypeptides would be expected to be useful in cancer therapy.

5 EXAMPLE 115: Induction of c-fos in Endothelial Cells (Assay 34)

This assay is designed to determine whether PRO polypeptides show the ability to induce c-fos in endothelial cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of conditions or disorders where angiogenesis would be beneficial including, for example, wound healing, and the like (as would agonists of these PRO polypeptides). Antagonists of the PRO
10 polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of cancerous tumors.

Human venous umbilical vein endothelial cells (HUVEC, Cell Systems) in growth media (50% Ham's F12 w/o GHT: low glucose, and 50% DMEM without glycine: with NaHCO₃, 1% glutamine, 10 mM HEPES, 10% FBS, 10 ng/ml bFGF) were plated on 96-well microtiter plates at a cell density of 1x10⁴ cells/well. The
15 day after plating, the cells were starved by removing the growth media and treating the cells with 100 μ l/well test samples and controls (positive control = growth media; negative control = Protein 32 buffer = 10 mM HEPES, 140 mM NaCl, 4% (w/v) mannitol, pH 6.8). The cells were incubated for 30 minutes at 37°C, in 5% CO₂. The samples were removed, and the first part of the bDNA kit protocol (Chiron Diagnostics, cat. #6005-037) was followed, where each capitalized reagent/buffer listed below was available from the kit.

20 Briefly, the amounts of the TM Lysis Buffer and Probes needed for the tests were calculated based on information provided by the manufacturer. The appropriate amounts of thawed Probes were added to the TM Lysis Buffer. The Capture Hybridization Buffer was warmed to room temperature. The bDNA strips were set up in the metal strip holders, and 100 μ l of Capture Hybridization Buffer was added to each b-DNA well needed, followed by incubation for at least 30 minutes. The test plates with the cells were removed from the incubator,
25 and the media was gently removed using the vacuum manifold. 100 μ l of Lysis Hybridization Buffer with Probes were quickly pipetted into each well of the microtiter plates. The plates were then incubated at 55°C for 15 minutes. Upon removal from the incubator, the plates were placed on the vortex mixer with the microtiter adapter head and vortexed on the #2 setting for one minute. 80 μ l of the lysate was removed and added to the bDNA wells containing the Capture Hybridization Buffer, and pipetted up and down to mix. The plates were
30 incubated at 53°C for at least 16 hours.

On the next day, the second part of the bDNA kit protocol was followed. Specifically, the plates were removed from the incubator and placed on the bench to cool for 10 minutes. The volumes of additions needed were calculated based upon information provided by the manufacturer. An Amplifier Working Solution was prepared by making a 1:100 dilution of the Amplifier Concentrate (20 fm/ μ l) in AL Hybridization Buffer. The
35 hybridization mixture was removed from the plates and washed twice with Wash A. 50 μ l of Amplifier Working Solution was added to each well and the wells were incubated at 53°C for 30 minutes. The plates were then removed from the incubator and allowed to cool for 10 minutes. The Label Probe Working Solution was

prepared by making a 1:100 dilution of Label Concentrate (40 pmoles/ μ l) in AL Hybridization Buffer. After the 10-minute cool-down period, the amplifier hybridization mixture was removed and the plates were washed twice with Wash A. 50 μ l of Label Probe Working Solution was added to each well and the wells were incubated at 53°C for 15 minutes. After cooling for 10 minutes, the Substrate was warmed to room temperature. Upon addition of 3 μ l of Substrate Enhancer to each ml of Substrate needed for the assay, the plates were
5 allowed to cool for 10 minutes, the label hybridization mixture was removed, and the plates were washed twice with Wash A and three times with Wash D. 50 μ l of the Substrate Solution with Enhancer was added to each well. The plates were incubated for 30 minutes at 37°C and RLU was read in an appropriate luminometer.

The replicates were averaged and the coefficient of variation was determined. The measure of activity of the fold increase over the negative control (Protein 32/HEPES buffer described above) value was indicated
10 by chemiluminescence units (RLU). The results are considered positive if the PRO polypeptide exhibits at least a two-fold value over the negative buffer control. Negative control = 1.00 RLU at 1.00% dilution. Positive control = 8.39 RLU at 1.00% dilution.

The following PRO polypeptides tested positive in this assay: PRO938, PRO200, PRO865, PRO788 and PRO1013.
15

EXAMPLE 116: Proliferation of Rat Utricular Supporting Cells (Assay 54)

This assay shows that certain polypeptides of the invention act as potent mitogens for inner ear supporting cells which are auditory hair cell progenitors and, therefore, are useful for inducing the regeneration of auditory hair cells and treating hearing loss in mammals. The assay is performed as follows. Rat UEC-4
20 utricular epithelial cells are aliquoted into 96 well plates with a density of 3000 cells/well in 200 μ l of serum-containing medium at 33°C. The cells are cultured overnight and are then switched to serum-free medium at 37°C. Various dilutions of PRO polypeptides (or nothing for a control) are then added to the cultures and the cells are incubated for 24 hours. After the 24 hour incubation, ³H-thymidine (1 μ Ci/well) is added and the cells are then cultured for an additional 24 hours. The cultures are then washed to remove unincorporated radiolabel,
25 the cells harvested and Cpm per well determined. Cpm of at least 30% or greater in the PRO polypeptide treated cultures as compared to the control cultures is considered a positive in the assay.

The following polypeptide tested positive in this assay: PRO337, PRO363 and PRO1012.

EXAMPLE 117: Detection of PRO Polypeptides That Affect Glucose or FFA Uptake by Primary Rat Adipocytes (Assay 94) 30

This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by adipocyte cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by adipocytes would be beneficial including, for example, obesity, diabetes or hyper- or hypo-insulinemia.

35 In a 96 well format, PRO polypeptides to be assayed are added to primary rat adipocytes, and allowed to incubate overnight. Samples are taken at 4 and 16 hours and assayed for glycerol, glucose and FFA uptake. After the 16 hour incubation, insulin is added to the media and allowed to incubate for 4 hours. At this time, a

sample is taken and glycerol, glucose and FFA uptake is measured. Media containing insulin without the PRO polypeptide is used as a positive reference control. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

The following PRO polypeptides tested positive as stimulators of glucose and/or FFA uptake in this assay: PRO181, PRO200, PRO337, PRO362, PRO363, PRO731, PRO534, PRO1114 and PRO1075.

The following PRO polypeptides tested positive as inhibitors of glucose and/or FFA uptake in this assay: PRO195, PRO322, PRO862, PRO868, PRO865 and PRO162.

10 EXAMPLE 118: Detection of Polypeptides That Affect Glucose and/or FFA Uptake in Skeletal Muscle (Assay 106)

This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by skeletal muscle cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by skeletal muscle would be beneficial including, for example, diabetes or hyper- or hypo-insulinemia.

15 In a 96 well format, PRO polypeptides to be assayed are added to primary rat differentiated skeletal muscle, and allowed to incubate overnight. Then fresh media with the PRO polypeptide and +/- insulin are added to the wells. The sample media is then monitored to determine glucose and FFA uptake by the skeletal muscle cells. The insulin will stimulate glucose and FFA uptake by the skeletal muscle, and insulin in media without the PRO polypeptide is used as a positive control, and a limit for scoring. As the PRO polypeptide being
20 tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

The following PRO polypeptides tested positive as either stimulators or inhibitors of glucose and/or FFA uptake in this assay: PRO181, PRO200, PRO1083, PRO865, PRO162, PRO1008 and PRO1330.

25 EXAMPLE 119: Stimulation of Heart Neonatal Hypertrophy (Assay 1)

This assay is designed to measure the ability of PRO polypeptides to stimulate hypertrophy of neonatal heart. PRO polypeptides testing positive in this assay are expected to be useful for the therapeutic treatment of various cardiac insufficiency disorders.

Cardiac myocytes from 1-day old Harlan Sprague Dawley rats were obtained. Cells (180 μ l at 7.5×10^4 /ml, serum <0.1%, freshly isolated) are added on day 1 to 96-well plates previously coated with DMEM/F12 + 4% FCS. Test samples containing the test PRO polypeptide or growth medium only (negative control) (20 μ l/well) are added directly to the wells on day 1. PGF (20 μ l/well) is then added on day 2 at final concentration of 10^{-6} M. The cells are then stained on day 4 and visually scored on day 5, wherein cells showing no increase in size as compared to negative controls are scored 0.0, cells showing a small to moderate increase in size as
35 compared to negative controls are scored 1.0 and cells showing a large increase in size as compared to negative controls are scored 2.0. A positive result in the assay is a score of 1.0 or greater.

The following polypeptides tested positive in this assay: PRO195, PRO200, PRO526 and PRO792.

EXAMPLE 120: Enhancement of Heart Neonatal Hypertrophy Induced by F2a (Assay 37)

This assay is designed to measure the ability of PRO polypeptides to stimulate hypertrophy of neonatal heart. PRO polypeptides testing positive in this assay are expected to be useful for the therapeutic treatment of various cardiac insufficiency disorders.

Cardiac myocytes from 1-day old Harlan Sprague Dawley rats were obtained. Cells ($180 \mu\text{l}$ at $7.5 \times 10^4/\text{ml}$, serum $<0.1\%$, freshly isolated) are added on day 1 to 96-well plates previously coated with DMEM/F12 + 4% FCS. Test samples containing the test PRO polypeptide ($20 \mu\text{l}/\text{well}$) are added directly to the wells on day 1. PGF ($20 \mu\text{l}/\text{well}$) is then added on day 2 at a final concentration of 10^{-6} M. The cells are then stained on day 4 and visually scored on day 5. Visual scores are based on cell size, wherein cells showing no increase in size as compared to negative controls are scored 0.0, cells showing a small to moderate increase in size as compared to negative controls are scored 1.0 and cells showing a large increase in size as compared to negative controls are scored 2.0. A score of 1.0 or greater is considered positive.

No PBS is included, since calcium concentration is critical for assay response. Plates are coated with DMEM/F12 plus 4% FCS ($200 \mu\text{l}/\text{well}$). Assay media included: DMEM/F12 (with 2.44 gm bicarbonate), $10 \mu\text{g}/\text{ml}$ transferrin, $1 \mu\text{g}/\text{ml}$ insulin, $1 \mu\text{g}/\text{ml}$ aprotinin, 2 mmol/L glutamine, 100 U/ml penicillin G, $100 \mu\text{g}/\text{ml}$ streptomycin. Protein buffer containing mannitol (4%) gave a positive signal (score 3.5) at 1/10 (0.4%) and 1/100 (0.04%), but not at 1/1000 (0.004%). Therefore the test sample buffer containing mannitol is not run.

The following PRO polypeptides tested positive in this assay: PRO195.

EXAMPLE 121: Guinea Pig Vascular Leak (Assays 32 and 51)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce vascular permeability. Polypeptides testing positive in this assay are expected to be useful for the therapeutic treatment of conditions which would benefit from enhanced vascular permeability including, for example, conditions which may benefit from enhanced local immune system cell infiltration.

Hairless guinea pigs weighing 350 grams or more were anesthetized with Ketamine (75-80 mg/kg) and 5 mg/kg Xylazine intramuscularly. Test samples containing the PRO polypeptide or a physiological buffer without the test polypeptide are injected into skin on the back of the test animals with $100 \mu\text{l}$ per injection site intradermally. There were approximately 16-24 injection sites per animal. One ml of Evans blue dye (1% in PBS) is then injected intracardially. Skin vascular permeability responses to the compounds (*i.e.*, blemishes at the injection sites of injection) are visually scored by measuring the diameter (in mm) of blue-colored leaks from the site of injection at 1 and 6 hours post administration of the test materials. The mm diameter of blueness at the site of injection is observed and recorded as well as the severity of the vascular leakage. Blemishes of at least 5 mm in diameter are considered positive for the assay when testing purified proteins, being indicative of the ability to induce vascular leakage or permeability. A response greater than 7 mm diameter is considered positive for conditioned media samples. Human VEGF at $0.1 \mu\text{g}/100 \mu\text{l}$ is used as a positive control, inducing a response of 15-23 mm diameter.

The following PRO polypeptides tested positive in this assay: PRO200.

EXAMPLE 122: Skin Vascular Permeability Assay (Assay 64)

This assay shows that certain polypeptides of the invention stimulate an immune response and induce inflammation by inducing mononuclear cell, eosinophil and PMN infiltration at the site of injection of the animal. Compounds which stimulate an immune response are useful therapeutically where stimulation of an immune response is beneficial. This skin vascular permeability assay is conducted as follows. Hairless guinea pigs weighing 350 grams or more are anesthetized with ketamine (75-80 mg/Kg) and 5 mg/Kg xylazine intramuscularly (IM). A sample of purified polypeptide of the invention or a conditioned media test sample is injected intradermally onto the backs of the test animals with 100 μ l per injection site. It is possible to have about 10-30, preferably about 16-24, injection sites per animal. One μ l of Evans blue dye (1% in physiologic buffered saline) is injected intracardially. Blemishes at the injection sites are then measured (mm diameter) at 1 hr and 6 hr post injection. Animals were sacrificed at 6 hrs after injection. Each skin injection site is biopsied and fixed in formalin. The skins are then prepared for histopathologic evaluation. Each site is evaluated for inflammatory cell infiltration into the skin. Sites with visible inflammatory cell inflammation are scored as positive. Inflammatory cells may be neutrophilic, eosinophilic, monocytic or lymphocytic. At least a minimal perivascular infiltrate at the injection site is scored as positive, no infiltrate at the site of injection is scored as negative.

The following polypeptide tested positive in this assay: PRO200, PRO362 and PRO1031.

EXAMPLE 123: Induction of c-fos in Cortical Neurons (Assay 83)

This assay is designed to determine whether PRO polypeptides show the ability to induce c-fos in cortical neurons. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of nervous system disorders and injuries where neuronal proliferation would be beneficial.

Cortical neurons are dissociated and plated in growth medium at 10,000 cells per well in 96 well plates. After approximately 2 cellular divisions, the cells are treated for 30 minutes with the PRO polypeptide or nothing (negative control). The cells are then fixed for 5 minutes with cold methanol and stained with an antibody directed against phosphorylated CREB. mRNA levels are then calculated using chemiluminescence. A positive in the assay is any factor that results in at least a 2-fold increase in c-fos message as compared to the negative controls.

The following PRO polypeptides tested positive in this assay: PRO200.

EXAMPLE 124: Mouse Kidney Mesangial Cell Proliferation Assay (Assay 92)

This assay shows that certain polypeptides of the invention act to induce proliferation of mammalian kidney mesangial cells and, therefore, are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with Schönlein-Henoch purpura, celiac disease, dermatitis herpetiformis or Crohn disease. The assay is performed as follows. On day one, mouse kidney mesangial cells are plated on a 96 well plate in growth media (3:1 mixture of Dulbecco's modified Eagle's medium and Ham's F12 medium, 95% fetal bovine serum, 5% supplemented with 14 mM HEPES) and grown overnight. On day 2, PRO polypeptides are diluted at 2 concentrations (1% and 0.1%) in serum-free

medium and added to the cells. Control samples are serum-free medium alone. On day 4, 20 μ l of the Cell Titer 96 Aqueous one solution reagent (Progenia) was added to each well and the colorimetric reaction was allowed to proceed for 2 hours. The absorbance (OD) is then measured at 490 nm. A positive in the assay is anything that gives an absorbance reading which is at least 15% above the control reading.

5 The following polypeptide tested positive in this assay: PRO200, PRO363, PRO731, PRO534, PRO866 and PRO1031.

EXAMPLE 125: Pericyte c-Fos Induction (Assay 93)

10 This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 100 μ l of PRO polypeptide test samples and controls (positive control = DME+5% serum +/- PDGF at 500 ng/ml; negative control = protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading verses frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media = low glucose DMEM = 20% FBS + 1X pen strep + 1X fungizone. Assay Media = low glucose DMEM +5% FBS.

20 The following polypeptides tested positive in this assay: PRO200.

EXAMPLE 126: Chondrocyte Re-differentiation Assay (Assay 110)

25 This assay shows that certain polypeptides of the invention act to induce redifferentiation of chondrocytes, therefore, are expected to be useful for the treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis. The assay is performed as follows. Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of metacarpophalangeal joints of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 μ g/ml gentamycin. The culture media is changed every third day and the cells are then seeded in 96 well plates at 5,000 cells/well in 100 μ l of the same media without serum and 100 μ l of the test PRO polypeptide, 5 nM staurosporin (positive control) or medium alone (negative control) is added to give a final volume of 200 μ l/well. After 5 days of incubation at 37°C, a picture of each well is taken and the differentiation state of the chondrocytes is determined. A positive result in the assay occurs when the redifferentiation of the chondrocytes is determined to be more similar to the positive control than the negative control.

35 The following polypeptide tested positive in this assay: PRO200, PRO285, PRO337, PRO526, PRO362, PRO363, PRO531, PRO1083, PRO862, PRO733, PRO1017, PRO792, PRO788, PRO1008, PRO1075, PRO725 and PRO1031.

EXAMPLE 127: Fetal Hemoglobin Induction in an Erythroblastic Cell Line (Assay 107)

This assay is useful for screening PRO polypeptides for the ability to induce the switch from adult hemoglobin to fetal hemoglobin in an erythroblastic cell line. Molecules testing positive in this assay are expected to be useful for therapeutically treating various mammalian hemoglobin-associated disorders such as the various thalassemias. The assay is performed as follows. Erythroblastic cells are plated in standard growth medium at 1000 cells/well in a 96 well format. PRO polypeptides are added to the growth medium at a concentration of 0.2% or 2% and the cells are incubated for 5 days at 37°C. As a positive control, cells are treated with 100μM hemin and as a negative control, the cells are untreated. After 5 days, cell lysates are prepared and analyzed for the expression of gamma globin (a fetal marker). A positive in the assay is a gamma globin level at least 2-fold above the negative control.

The following polypeptides tested positive in this assay: PRO237, PRO381, PRO362, PRO724, PRO866, PRO1114, PRO725 and PRO1071.

EXAMPLE 128: Induction of Pancreatic β-Cell Precursor Proliferation (Assay 117)

This assay shows that certain polypeptides of the invention act to induce an increase in the number of pancreatic β-cell precursor cells and, therefore, are useful for treating various insulin deficient states in mammals, including diabetes mellitus. The assay is performed as follows. The assay uses a primary culture of mouse fetal pancreatic cells and the primary readout is an alteration in the expression of markers that represent either β-cell precursors or mature β-cells. Marker expression is measured by real time quantitative PCR (RTQ-PCR); wherein the marker being evaluated is a transcription factor called Pdx1.

The pancreata are dissected from E14 embryos (CD1 mice). The pancreata are then digested with collagenase/dispase in F12/DMEM at 37°C for 40 to 60 minutes (collagenase/dispase, 1.37 mg/ml, Boehringer Mannheim, #1097113). The digestion is then neutralized with an equal volume of 5% BSA and the cells are washed once with RPMI1640. At day 1, the cells are seeded into 12-well tissue culture plates (pre-coated with laminin, 20μg/ml in PBS, Boehringer Mannheim, #124317). Cells from pancreata from 1-2 embryos are distributed per well. The culture medium for this primary culture is 14F/1640. At day 2, the media is removed and the attached cells washed with RPMI/1640. Two mls of minimal media are added in addition to the protein to be tested. At day 4, the media is removed and RNA prepared from the cells and marker expression analyzed by real time quantitative RT-PCR. A protein is considered to be active in the assay if it increases the expression of the relevant β-cell marker as compared to untreated controls.

14F/1640 is RPMI1640 (Gibco) plus the following:

group A 1:1000

group B 1:1000

recombinant human insulin 10 μg/ml

Aprotinin (50μg/ml) 1:2000 (Boehringer manheim #981532)

Bovine pituitary extract (BPE) 60μg/ml

Gentamycin 100 ng/ml

Group A : (in 10ml PBS)

Transferrin, 100mg (Sigma T2252)

Epidermal Growth Factor, 100 μ g (BRL 100004)

Triiodothyronine, 10 μ l of 5x10⁻⁶ M (Sigma T5516)

Ethanolamine, 100 μ l of 10⁻¹ M (Sigma E0135)

5 Phosphoethalamine, 100 μ l of 10⁻¹ M (Sigma P0503)

Selenium, 4 μ l of 10⁻¹ M (Aesar #12574)

Group C : (in 10ml 100% ethanol)

Hydrocortisone, 2 μ l of 5X10⁻³ M (Sigma #H0135)

Progesterone, 100 μ l of 1X10⁻³ M (Sigma #P6149)

10 Forskolin, 500 μ l of 20mM (Calbiochem #344270)

Minimal media:

RPMI 1640 plus transferrin (10 μ g/ml), insulin (1 μ g/ml), gentamycin (100 ng/ml), aprotinin (50 μ g/ml) and BPE (15 μ g/ml).

Defined media:

15 RPMI 1640 plus transferrin (10 μ g/ml), insulin (1 μ g/ml), gentamycin (100 ng/ml) and aprotinin (50 μ g/ml).

The following polypeptides tested positive in this assay: PRO237 and PRO731.

EXAMPLE 129: Stimulatory Activity in Mixed Lymphocyte Reaction (MLR) Assay (Assay 24)

20 This example shows that certain polypeptides of the invention are active as a stimulator of the proliferation of stimulated T-lymphocytes. Compounds which stimulate proliferation of lymphocytes are useful therapeutically where enhancement of an immune response is beneficial. A therapeutic agent may take the form of antagonists of the polypeptide of the invention, for example, murine-human chimeric, humanized or human antibodies against the polypeptide.

25 The basic protocol for this assay is described in Current Protocols in Immunology, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, Published by John Wiley & Sons, Inc.

More specifically, in one assay variant, peripheral blood mononuclear cells (PBMC) are isolated from mammalian individuals, for example a human volunteer, by leukopheresis (one donor will supply stimulator PBMCs, the other donor will supply responder PBMCs). If desired, the cells are frozen in fetal bovine serum and DMSO after isolation. Frozen cells may be thawed overnight in assay media (37°C, 5% CO₂) and then washed and resuspended to 3x10⁶ cells/ml of assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate). The stimulator PBMCs are prepared by irradiating the cells (about 3000 Rads).

35 The assay is prepared by plating in triplicate wells a mixture of:

100:1 of test sample diluted to 1% or to 0.1%,

50 :1 of irradiated stimulator cells, and

50 :1 of responder PBMC cells.

100 microliters of cell culture media or 100 microliter of CD4-IgG is used as the control. The wells are then incubated at 37°C, 5% CO₂ for 4 days. On day 5, each well is pulsed with tritiated thymidine (1.0 mC/well; Amersham). After 6 hours the cells are washed 3 times and then the uptake of the label is evaluated.

In another variant of this assay, PBMCs are isolated from the spleens of Balb/c mice and C57B6 mice.

- 5 The cells are teased from freshly harvested spleens in assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate) and the PBMCs are isolated by overlaying these cells over Lympholyte M (Organon Teknika), centrifuging at 2000 rpm for 20 minutes, collecting and washing the mononuclear cell layer in assay media and resuspending the cells to 1x10⁷ cells/ml of assay media. The assay is then conducted as described above.

- 10 Positive increases over control are considered positive with increases of greater than or equal to 180% being preferred. However, any value greater than control indicates a stimulatory effect for the test protein.

The following PRO polypeptides tested positive in this assay: PRO273, PRO526, PRO381, PRO719, PRO866 and PRO1031.

15 EXAMPLE 130: Inhibitory Activity in Mixed Lymphocyte Reaction (MLR) Assay (Assay 67)

This example shows that one or more of the polypeptides of the invention are active as inhibitors of the proliferation of stimulated T-lymphocytes. Compounds which inhibit proliferation of lymphocytes are useful therapeutically where suppression of an immune response is beneficial.

- 20 The basic protocol for this assay is described in Current Protocols in Immunology, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, Published by John Wiley & Sons, Inc.

- 25 More specifically, in one assay variant, peripheral blood mononuclear cells (PBMC) are isolated from mammalian individuals, for example a human volunteer, by leukopheresis (one donor will supply stimulator PBMCs, the other donor will supply responder PBMCs). If desired, the cells are frozen in fetal bovine serum and DMSO after isolation. Frozen cells may be thawed overnight in assay media (37°C, 5% CO₂) and then washed and resuspended to 3x10⁶ cells/ml of assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate). The stimulator PBMCs are prepared by irradiating the cells (about 3000 Rads).

The assay is prepared by plating in triplicate wells a mixture of:

- 30 100:1 of test sample diluted to 1% or to 0.1%,
50 :1 of irradiated stimulator cells, and
50 :1 of responder PBMC cells.

- 35 100 microliters of cell culture media or 100 microliter of CD4-IgG is used as the control. The wells are then incubated at 37°C, 5% CO₂ for 4 days. On day 5, each well is pulsed with tritiated thymidine (1.0 mC/well; Amersham). After 6 hours the cells are washed 3 times and then the uptake of the label is evaluated.

In another variant of this assay, PBMCs are isolated from the spleens of Balb/c mice and C57B6 mice. The cells are teased from freshly harvested spleens in assay media (RPMI; 10% fetal bovine serum, 1%

penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate) and the PBMCs are isolated by overlaying these cells over Lympholyte M (Organon Teknika), centrifuging at 2000 rpm for 20 minutes, collecting and washing the mononuclear cell layer in assay media and resuspending the cells to 1×10^7 cells/ml of assay media. The assay is then conducted as described above.

Any decreases below control is considered to be a positive result for an inhibitory compound, with decreases of less than or equal to 80% being preferred. However, any value less than control indicates an inhibitory effect for the test protein.

The following polypeptide tested positive in this assay: PRO273, PRO526, PRO381, PRO701, PRO363, PRO531, PRO1083, PRO865, PRO788 and PRO1114.

10 EXAMPLE 131: Fibroblast (BHK-21) Proliferation (Assay 98)

This assay shows that certain PRO polypeptides of the invention act to induce proliferation of mammalian fibroblast cells in culture and, therefore, function as useful growth factors in mammalian systems. The assay is performed as follows. BHK-21 fibroblast cells plated in standard growth medium at 2500 cells/well in a total volume of 100 μ l. The PRO polypeptide, β -FGF (positive control) or nothing (negative control) are then added to the wells in the presence of 1 μ g/ml of heparin for a total final volume of 200 μ l. The cells are then incubated at 37°C for 6 to 7 days. After incubation, the media is removed, the cells are washed with PBS and then an acid phosphatase substrate reaction mixture (100 μ l/well) is added. The cells are then incubated at 37°C for 2 hours. 10 μ l per well of 1N NaOH is then added to stop the acid phosphatase reaction. The plates are then read at OD 405nm. A positive in the assay is acid phosphatase activity which is at least 50% above the negative control.

The following PRO polypeptide tested positive in this assay: PRO273 and PRO731.

EXAMPLE 132: Induction of Endothelial Cell Apoptosis (ELISA) (Assay 109)

The ability of PRO polypeptides to induce apoptosis in endothelial cells was tested in human venous umbilical vein endothelial cells (HUVEC, Cell Systems) using a 96-well format, in 0% serum media supplemented with 100 ng/ml VEGF, 0.1% BSA, 1X penn/strep. A positive result in this assay indicates the usefulness of the polypeptide for therapeutically treating any of a variety of conditions associated with undesired endothelial cell growth including, for example, the inhibition of tumor growth. The 96-well plates used were manufactured by Falcon (No. 3072). Coating of 96 well plates were prepared by allowing gelatinization to occur for >30 minutes with 100 μ l of 0.2% gelatin in PBS solution. The gelatin mix was aspirated thoroughly before plating HUVEC cells at a final concentration of 2×10^4 cells/ml in 10% serum containing medium - 100 μ l volume per well. The cells were grown for 24 hours before adding test samples containing the PRO polypeptide of interest.

To all wells, 100 μ l of 0% serum media (Cell Systems) complemented with 100 ng/ml VEGF, 0.1% BSA, 1X penn/strep was added. Test samples containing PRO polypeptides were added in triplicate at dilutions of 1%, 0.33% and 0.11%. Wells without cells were used as a blank and wells with cells only were used as a negative control. As a positive control, 1:3 serial dilutions of 50 μ l of a 3x stock of staurosporine were used.

The cells were incubated for 24 to 35 hours prior to ELISA.

ELISA was used to determine levels of apoptosis preparing solutions according to the Boehringer Manual [Boehringer, Cell Death Detection ELISA plus, Cat No. 1 920 685]. Sample preparations: 96 well plates were spun down at 1 krpm for 10 minutes (200g); the supernatant was removed by fast inversion, placing the plate upside down on a paper towel to remove residual liquid. To each well, 200 μ l of 1X Lysis buffer was added and incubation allowed at room temperature for 30 minutes without shaking. The plates were spun down for 10 minutes at 1 krpm, and 20 μ l of the lysate (cytoplasmic fraction) was transferred into streptavidin coated MTP. 80 μ l of immunoreagent mix was added to the 20 μ l lysate in each well. The MTP was covered with adhesive foil and incubated at room temperature for 2 hours by placing it on an orbital shaker (200 rpm). After two hours, the supernatant was removed by suction and the wells rinsed three times with 250 μ l of 1X incubation buffer per well (removed by suction). Substrate solution was added (100 μ l) into each well and incubated on an orbital shaker at room temperature at 250 rpm until color development was sufficient for a photometric analysis (approx. after 10-20 minutes). A 96 well reader was used to read the plates at 405 nm, reference wavelength, 492 nm. The levels obtained for PIN 32 (control buffer) was set to 100%. Samples with levels > 130% were considered positive for induction of apoptosis.

The following PRO polypeptides tested positive in this assay: PRO846.

EXAMPLE 133: Induction of Endothelial Cell Apoptosis (Assay 73)

The ability of PRO polypeptides to induce apoptosis in endothelial cells was tested in human venous umbilical vein endothelial cells (HUVEC, Cell Systems). A positive test in the assay is indicative of the usefulness of the polypeptide in therapeutically treating tumors as well as vascular disorders where inducing apoptosis of endothelial cells would be beneficial.

The cells were plated on 96-well microtiter plates (Amersham Life Science, cytostar-T scintillating microplate, RPNQ160, sterile, tissue-culture treated, individually wrapped), in 10% serum (CSG-medium, Cell Systems), at a density of 2×10^4 cells per well in a total volume of 100 μ l. On day 2, test samples containing the PRO polypeptide were added in triplicate at dilutions of 1%, 0.33% and 0.11%. Wells without cells were used as a blank and wells with cells only were used as a negative control. As a positive control 1:3 serial dilutions of 50 μ l of a 3x stock of staurosporine were used. The ability of the PRO polypeptide to induce apoptosis was determined by processing of the 96 well plates for detection of Annexin V, a member of the calcium and phospholipid binding proteins, to detect apoptosis.

0.2 ml Annexin V - Biotin stock solution (100 μ g/ml) was diluted in 4.6 ml $2 \times \text{Ca}^{2+}$ binding buffer and 2.5% BSA (1:25 dilution). 50 μ l of the diluted Annexin V - Biotin solution was added to each well (except controls) to a final concentration of 1.0 μ g/ml. The samples were incubated for 10-15 minutes with Annexin-Biotin prior to direct addition of ^{35}S -Streptavidin. ^{35}S -Streptavidin was diluted in $2 \times \text{Ca}^{2+}$ Binding buffer, 2.5% BSA and was added to all wells at a final concentration of 3×10^4 cpm/well. The plates were then sealed, centrifuged at 1000 rpm for 15 minutes and placed on orbital shaker for 2 hours. The analysis was performed on a 1450 Microbeta Trilux (Wallac). Percent above background represents the percentage amount of counts per minute above the negative controls. Percents greater than or equal to 30% above background are considered

positive.

The following PRO polypeptides tested positive in this assay: PRO719.

EXAMPLE 134: Human Venous Endothelial Cell Calcium Flux Assay (Assay 68)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to stimulate calcium flux in human umbilical vein endothelial cells (HUVEC, Cell Systems). Calcium influx is a well documented response upon binding of certain ligands to their receptors. A test compound that results in a positive response in the present calcium influx assay can be said to bind to a specific receptor and activate a biological signaling pathway in human endothelial cells. This could ultimately lead, for example, to endothelial cell division, inhibition of endothelial cell proliferation, endothelial tube formation, cell migration, apoptosis, etc.

Human venous umbilical vein endothelial cells (HUVEC, Cell Systems) in growth media (50:50 without glycine, 1% glutamine, 10mM Hepes, 10% FBS, 10 ng/ml bFGF), were plated on 96-well microtiter ViewPlates-96 (Packard Instrument Company Part #6005182) microtiter plates at a cell density of 2×10^4 cells/well. The day after plating, the cells were washed three times with buffer (HBSS plus 10 mM Hepes), leaving 100 μ l/well. Then 100 μ l/well of 8 μ M Fluo-3 (2x) was added. The cells were incubated for 1.5 hours at 37°C/5% CO₂. After incubation, the cells were then washed 3x with buffer (described above) leaving 100 μ l/well. Test samples of the PRO polypeptides were prepared on different 96-well plates at 5x concentration in buffer. The positive control corresponded to 50 μ M ionomycin (5x); the negative control corresponded to Protein 32. Cell plate and sample plates were run on a FLIPR (Molecular Devices) machine. The FLIPR machine added 25 μ l of test sample to the cells, and readings were taken every second for one minute, then every 3 seconds for the next three minutes.

The fluorescence change from baseline to the maximum rise of the curve (Δ change) was calculated, and replicates averaged. The rate of fluorescence increase was monitored, and only those samples which had a Δ change greater than 1000 and a rise within 60 seconds, were considered positive.

The following PRO polypeptides tested positive in the present assay: PRO771.

EXAMPLE 135: Induction of c-fos in Endothelial Cells (Assay 34)

This assay is designed to determine whether PRO polypeptides show the ability to induce c-fos in endothelial cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of conditions or disorders where angiogenesis would be beneficial including, for example, wound healing, and the like (as would agonists of these PRO polypeptides). Antagonists of the PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of cancerous tumors.

Human venous umbilical vein endothelial cells (HUVEC, Cell Systems) in growth media (50% Ham's F12 w/o GHT: low glucose, and 50% DMEM without glycine: with NaHCO₃, 1% glutamine, 10 mM HEPES, 10% FBS, 10 ng/ml bFGF) were plated on 96-well microtiter plates at a cell density of 1×10^4 cells/well. The day after plating, the cells were starved by removing the growth media and treating the cells with 100 μ l/well

test samples and controls (positive control = growth media; negative control = Protein 32 buffer = 10 mM HEPES, 140 mM NaCl, 4% (w/v) mannitol, pH 6.8). The cells were incubated for 30 minutes at 37°C, in 5% CO₂. The samples were removed, and the first part of the bDNA kit protocol (Chiron Diagnostics, cat. #6005-037) was followed, where each capitalized reagent/buffer listed below was available from the kit.

5 Briefly, the amounts of the TM Lysis Buffer and Probes needed for the tests were calculated based on information provided by the manufacturer. The appropriate amounts of thawed Probes were added to the TM Lysis Buffer. The Capture Hybridization Buffer was warmed to room temperature. The bDNA strips were set up in the metal strip holders, and 100 µl of Capture Hybridization Buffer was added to each b-DNA well needed, followed by incubation for at least 30 minutes. The test plates with the cells were removed from the incubator, and the media was gently removed using the vacuum manifold. 100 µl of Lysis Hybridization Buffer with
10 Probes were quickly pipetted into each well of the microtiter plates. The plates were then incubated at 55°C for 15 minutes. Upon removal from the incubator, the plates were placed on the vortex mixer with the microtiter adapter head and vortexed on the #2 setting for one minute. 80 µl of the lysate was removed and added to the bDNA wells containing the Capture Hybridization Buffer, and pipetted up and down to mix. The plates were incubated at 53°C for at least 16 hours.

15 On the next day, the second part of the bDNA kit protocol was followed. Specifically, the plates were removed from the incubator and placed on the bench to cool for 10 minutes. The volumes of additions needed were calculated based upon information provided by the manufacturer. An Amplifier Working Solution was prepared by making a 1:100 dilution of the Amplifier Concentrate (20 fm/µl) in AL Hybridization Buffer. The hybridization mixture was removed from the plates and washed twice with Wash A. 50 µl of Amplifier Working
20 Solution was added to each well and the wells were incubated at 53°C for 30 minutes. The plates were then removed from the incubator and allowed to cool for 10 minutes. The Label Probe Working Solution was prepared by making a 1:100 dilution of Label Concentrate (40 pmoles/µl) in AL Hybridization Buffer. After the 10-minute cool-down period, the amplifier hybridization mixture was removed and the plates were washed twice with Wash A. 50 µl of Label Probe Working Solution was added to each well and the wells were
25 incubated at 53°C for 15 minutes. After cooling for 10 minutes, the Substrate was warmed to room temperature. Upon addition of 3 µl of Substrate Enhancer to each ml of Substrate needed for the assay, the plates were allowed to cool for 10 minutes, the label hybridization mixture was removed, and the plates were washed twice with Wash A and three times with Wash D. 50 µl of the Substrate Solution with Enhancer was added to each well. The plates were incubated for 30 minutes at 37°C and RLU was read in an appropriate luminometer.

30 The replicates were averaged and the coefficient of variation was determined. The measure of activity of the fold increase over the negative control (Protein 32/HEPES buffer described above) value was indicated by chemiluminescence units (RLU). The results are considered positive if the PRO polypeptide exhibits at least a two-fold value over the negative buffer control. Negative control = 1.00 RLU at 1.00% dilution. Positive control = 8.39 RLU at 1.00% dilution.

35 The following PRO polypeptides tested positive in this assay: PRO474.

EXAMPLE 136: Induction of Pancreatic β -Cell Precursor Differentiation (Assay 89)

This assay shows that certain polypeptides of the invention act to induce differentiation of pancreatic β -cell precursor cells into mature pancreatic β -cells and, therefore, are useful for treating various insulin deficient states in mammals, including diabetes mellitus. The assay is performed as follows. The assay uses a primary culture of mouse fetal pancreatic cells and the primary readout is an alteration in the expression of markers that represent either β -cell precursors or mature β -cells. Marker expression is measured by real time quantitative PCR (RTQ-PCR); wherein the marker being evaluated is insulin.

The pancreata are dissected from E14 embryos (CD1 mice). The pancreata are then digested with collagenase/dispase in F12/DMEM at 37°C for 40 to 60 minutes (collagenase/dispase, 1.37 mg/ml, Boehringer Mannheim, #1097113). The digestion is then neutralized with an equal volume of 5% BSA and the cells are washed once with RPMI1640. At day 1, the cells are seeded into 12-well tissue culture plates (pre-coated with laminin, 20 μ g/ml in PBS, Boehringer Mannheim, #124317). Cells from pancreata from 1-2 embryos are distributed per well. The culture medium for this primary culture is 14F/1640. At day 2, the media is removed and the attached cells washed with RPMI/1640. Two mls of minimal media are added in addition to the protein to be tested. At day 4, the media is removed and RNA prepared from the cells and marker expression analyzed by real time quantitative RT-PCR. A protein is considered to be active in the assay if it increases the expression of the relevant β -cell marker as compared to untreated controls.

14F/1640 is RPMI1640 (Gibco) plus the following:

- group A 1:1000
- group B 1:1000
- recombinant human insulin 10 μ g/ml
- Aprotinin (50 μ g/ml) 1:2000 (Boehringer manheim #981532)
- Bovine pituitary extract (BPE) 60 μ g/ml
- Gentamycin 100 ng/ml

Group A : (in 10ml PBS)

- Transferrin, 100mg (Sigma T2252)
- Epidermal Growth Factor, 100 μ g (BRL 100004)
- Triiodothyronine, 10 μ l of 5 $\times 10^{-6}$ M (Sigma T5516)
- Ethanolamine, 100 μ l of 10 $^{-1}$ M (Sigma E0135)
- Phosphoethalamine, 100 μ l of 10 $^{-1}$ M (Sigma P0503)
- Selenium, 4 μ l of 10 $^{-1}$ M (Aesar #12574)

Group C : (in 10ml 100% ethanol)

- Hydrocortisone, 2 μ l of 5 $\times 10^{-3}$ M (Sigma #H0135)
- Progesterone, 100 μ l of 1 $\times 10^{-3}$ M (Sigma #P6149)
- Forskolin, 500 μ l of 20mM (Calbiochem #344270)

Minimal media:

RPMI 1640 plus transferrin (10 μ g/ml), insulin (1 μ g/ml), gentamycin (100 ng/ml), aprotinin (50 μ g/ml) and BPE (15 μ g/ml).

Defined media:

RPMI 1640 plus transferrin (10 $\mu\text{g/ml}$), insulin (1 $\mu\text{g/ml}$), gentamycin (100 ng/ml) and aprotinin (50 $\mu\text{g/ml}$).

The following polypeptides were positive in this assay: PRO788 and PRO162.

5 EXAMPLE 137: Stimulation of Endothelial Cell Proliferation (Assay 8)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to stimulate adrenal cortical capillary endothelial cell (ACE) growth. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of conditions or disorders where angiogenesis would be beneficial including, for example, wound healing, and the like (as would agonists of these PRO polypeptides). Antagonists of the PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of cancerous tumors.

Bovine adrenal cortical capillary endothelial (ACE) cells (from primary culture, maximum of 12-14 passages) were plated in 96-well plates at 500 cells/well per 100 microliter. Assay media included low glucose DMEM, 10% calf serum, 2 mM glutamine, and 1X penicillin/streptomycin/fungizone. Control wells included the following: (1) no ACE cells added; (2) ACE cells alone; (3) ACE cells plus VEGF (5 ng/ml); and (4) ACE cells plus FGF (5 ng/ml). The control or test sample, (in 100 microliter volumes), was then added to the wells (at dilutions of 1%, 0.1% and 0.01%, respectively). The cell cultures were incubated for 6-7 days at 37°C/5% CO₂. After the incubation, the media in the wells was aspirated, and the cells were washed 1X with PBS. An acid phosphatase reaction mixture (100 microliter; 0.1M sodium acetate, pH 5.5, 0.1% Triton X-100, 10 mM p-nitrophenyl phosphate) was then added to each well. After a 2 hour incubation at 37°C, the reaction was stopped by addition of 10 microliters 1N NaOH. Optical density (OD) was measured on a microplate reader at 405 nm.

The activity of a PRO polypeptide was calculated as the fold increase in proliferation (as determined by the acid phosphatase activity, OD 405 nm) relative to (1) cell only background, and (2) relative to maximum stimulation by VEGF. VEGF (at 3-10 ng/ml) and FGF (at 1-5 ng/ml) were employed as an activity reference for maximum stimulation. Results of the assay were considered "positive" if the observed stimulation was \geq 50% increase over background. VEGF (5 ng/ml) control at 1% dilution gave 1.24 fold stimulation; FGF (5 ng/ml) control at 1% dilution gave 1.46 fold stimulation.

The following PRO polypeptides tested positive in this assay: PRO1075.

30 EXAMPLE 138: Mouse Mesengial Cell Inhibition Assay (Assay 114)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to inhibit the proliferation of mouse mesengial cells in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of such diseases or conditions where inhibition of mesengial cell proliferation would be beneficial such as, for example, cystic renal dysplasia, polycystic kidney disease, or other kidney disease associated with abnormal mesengial cell proliferation, renal tumors, and the like.

On day 1, mouse mesengial cells are plated on a 96 well plate in growth medium (a 3:1 mixture of Dulbecco's modified Eagle's medium and Ham's F12 medium, 95 %; fetal bovine serum, 5 %; supplemented with 14mM HEPES) and then are allowed to grow overnight. On day 2, the PRO polypeptide is diluted at 2 different concentrations (1%, 0.1%) in serum-free medium and is added to the cells. The negative control is growth medium without added PRO polypeptide. After the cells are allowed to incubate for 48 hours, 20 μ l of the Cell
5 Titer 96 Aqueous one solution reagent (Promega) is added to each well and the colormetric reaction is allowed to proceed for 2 hours. The absorbance (OD) is then measured at 490 nm. A positive in the assay is an absorbance reading which is at least 10% above the negative control.

The following PRO polypeptides tested positive in this assay: PRO200 and PRO697.

10 EXAMPLE 139: Chondrocyte Proliferation Assay (Assay 111)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

15 Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 μ g/ml gentamycin. The culture media is changed every third day and the cells are reseeded to 25,000 cells/cm² every five days. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100 μ l of the same media without serum and 100 μ l of either serum-free medium (negative
20 control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 μ l/well. After 5 days at 37°C, 20 μ l of Alamar blue is added to each well and the plates are incubated for an additional 3 hours at 37°C. The fluorescence is then measured in each well (Ex:530 nm; Em: 590 nm). The fluorescence of a plate containing 200 μ l of the serum-free medium is measured to obtain the background. A positive result in the assay is obtained when the fluorescence of the PRO polypeptide
25 treated sample is more like that of the positive control than the negative control.

The following PRO polypeptides tested positive in this assay: PRO181, PRO200 and PRO322.

EXAMPLE 140: Rat DRG Neuronal Survival Inhibition Assay

This assay is designed to determine whether PRO polypeptides of the present invention show the ability
30 to inhibit the survival of neural cells in culture. Polypeptides testing positive in this assay are expected to be useful for the therapeutic treatment of neuropathic conditions which are associated with undesirable neural cell proliferation including, for example, neuroblastomas, gliomas, glioblastomas, and the like.

A heterogeneous population of neural cells freshly isolated from E14 rat embryo dorsal root ganglia are diluted in complete medium and are plated at 5,000 cells/well on polyurethane pretreated plates containing 50 μ l
35 F12 complete media. Test PRO polypeptides (50 μ l, one concentration) with 50 μ l additional assay media are then added to test for survival inhibition activity. Negative controls are treated with 100 μ l of complete medium alone. After 3 days incubation, the cells are stained with CMFDA and fixed after 1 hour with 4%

paraformaldehyde. Cells are then quantified by NIH image analysis. A positive in the assay is cell numbers in the treated well(s) being less than 0.5 of the untreated control well(s).

The following PRO polypeptides tested positive in this assay: PRO195 and PRO701.

EXAMPLE 141: Tissue Expression Distribution

- 5 Oligonucleotide probes were constructed from some of the PRO polypeptide-encoding nucleotide sequences shown in the accompanying figures for use in quantitative PCR amplification reactions. The oligonucleotide probes were chosen so as to give an approximately 200-600 base pair amplified fragment from the 3' end of its associated template in a standard PCR reaction. The oligonucleotide probes were employed in standard quantitative PCR amplification reactions with cDNA libraries isolated from different human adult and/or fetal tissue sources and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the PRO polypeptide-encoding nucleic acid in the various tissues tested. Knowledge of the expression pattern or the differential expression of the PRO polypeptide-encoding nucleic acid in various different human tissue types provides a diagnostic marker useful for tissue typing, with or without other tissue-specific markers, for determining the primary tissue source of a metastatic tumor, and the like. These assays provided the following results.

	<u>DNA Molecule</u>	<u>Tissues With Significant Expression</u>	<u>Tissues Lacking Significant Expression</u>
	DNA40954-1233	liver, lung	brain
	DNA41404-1352	lung, kidney	liver, retina, pancreas
	DNA44179-1362	liver	lung, brain
20	DNA45234-1277	kidney	liver, placenta, brain
	DNA45415-1318	thyroid, brain, kidney	liver, bone marrow
	DNA45417-1432	thyroid, brain, kidney, bone marrow	liver
	DNA45493-1349	liver, kidney	brain
	DNA48306-1291	brain, kidney	pancreas, liver
25	DNA48328-1355	thyroid, brain, liver, kidney	bone marrow
	DNA48329-1290	brain, bone marrow, kidney	liver, thyroid
	DNA49624-1279	placenta	liver, lung, kidney, brain
	DNA50911-1288	brain	placenta
	DNA50914-1289	brain, kidney, liver	placenta
30	DNA53906-1368	lung, kidney	brain
	DNA53912-1457	lung, liver, kidney, pancreas	brain
	DNA53977-1371	lung, liver, kidney, bone marrow	brain, pancreas
	DNA54002-1367	bone marrow, liver, kidney	lung, thyroid, brain
	DNA55737-1345	bone marrow, kidney	liver, brain
35	DNA57039-1402	pigment epithelium	lung, brain, liver, kidney
	DNA57253-1382	lung, brain, liver, kidney	placenta
	DNA58747-1384	lung, brain, kidney, liver	pancreas, thyroid
	DNA23318-1211	spleen, brain, heart, colon tumor, prostate	cartilage
	DNA39975-1210	brain, colon tumor, heart	THP-1 macrophages
40	DNA39979-1213	dendrocytes, cartilage, heart	spleen, substantia nigra, uterus, prostate
	DNA41386-1316	HUVEC, cartilage, dendrocytes	substantia nigra, colon tumor, uterus
	DNA50919-1361	HUVEC, brain, spleen, colon tumor	prostate, cartilage, heart, uterus
	DNA52185-1370	dendrocytes	substantia nigra, hippocampus, uterus
	DNA42663-1154	uterus, spleen, bone marrow	cartilage, HUVEC, colon tumor
45	DNA50980-1286	placenta, adrenal gland, prostate	bone marrow, uterus, cartilage

EXAMPLE 142: *In situ* Hybridization

In situ hybridization is a powerful and versatile technique for the detection and localization of nucleic acid sequences within cell or tissue preparations. It may be useful, for example, to identify sites of gene expression, analyze the tissue distribution of transcription, identify and localize viral infection, follow changes in specific mRNA synthesis and aid in chromosome mapping.

- 5 *In situ* hybridization was performed following an optimized version of the protocol by Lu and Gillett, Cell Vision 1:169-176 (1994), using PCR-generated ³³P-labeled riboprobes. Briefly, formalin-fixed, paraffin-embedded human tissues were sectioned, deparaffinized, deproteinized in proteinase K (20 g/ml) for 15 minutes at 37°C, and further processed for *in situ* hybridization as described by Lu and Gillett, *supra*. A [³³-P] UTP-labeled antisense riboprobe was generated from a PCR product and hybridized at 55°C overnight. The slides
10 were dipped in Kodak NTB2 nuclear track emulsion and exposed for 4 weeks.

³³P-Riboprobe synthesis

6.0 µl (125 mCi) of ³³P-UTP (Amersham BF 1002, SA < 2000 Ci/mmol) were speed vac dried. To each tube containing dried ³³P-UTP, the following ingredients were added:

- 2.0 µl 5x transcription buffer
15 1.0 µl DTT (100 mM)
2.0 µl NTP mix (2.5 mM : 10 µ; each of 10 mM GTP, CTP & ATP + 10 µl H₂O)
1.0 µl UTP (50 µM)
1.0 µl Rnasin
1.0 µl DNA template (1 µg)
20 1.0 µl H₂O
1.0 µl RNA polymerase (for PCR products T3 = AS, T7 = S, usually)

- The tubes were incubated at 37°C for one hour. 1.0 µl RQ1 DNase were added, followed by incubation at 37°C for 15 minutes. 90 µl TE (10 mM Tris pH 7.6/1mM EDTA pH 8.0) were added, and the mixture was pipetted onto DE81 paper. The remaining solution was loaded in a Microcon-50 ultrafiltration unit, and spun
25 using program 10 (6 minutes). The filtration unit was inverted over a second tube and spun using program 2 (3 minutes). After the final recovery spin, 100 µl TE were added. 1 µl of the final product was pipetted on DE81 paper and counted in 6 ml of Biofluor II.

- The probe was run on a TBE/urea gel. 1-3 µl of the probe or 5 µl of RNA Mrk III were added to 3 µl of loading buffer. After heating on a 95°C heat block for three minutes, the gel was immediately placed on
30 ice. The wells of gel were flushed, the sample loaded, and run at 180-250 volts for 45 minutes. The gel was wrapped in saran wrap and exposed to XAR film with an intensifying screen in -70°C freezer one hour to overnight.

³³P-HybridizationA. Pretreatment of frozen sections

- 35 The slides were removed from the freezer, placed on aluminium trays and thawed at room temperature for 5 minutes. The trays were placed in 55°C incubator for five minutes to reduce condensation. The slides were fixed for 10 minutes in 4% paraformaldehyde on ice in the fume hood, and washed in 0.5 x SSC for 5

minutes, at room temperature (25 ml 20 x SSC + 975 ml SQ H₂O). After deproteinization in 0.5 µg/ml proteinase K for 10 minutes at 37°C (12.5 µl of 10 mg/ml stock in 250 ml prewarmed RNase-free RNase buffer), the sections were washed in 0.5 x SSC for 10 minutes at room temperature. The sections were dehydrated in 70%, 95%, 100% ethanol, 2 minutes each.

B. Pretreatment of paraffin-embedded sections

5 The slides were deparaffinized, placed in SQ H₂O, and rinsed twice in 2 x SSC at room temperature, for 5 minutes each time. The sections were deproteinated in 20 µg/ml proteinase K (500 µl of 10 mg/ml in 250 ml RNase-free RNase buffer; 37°C, 15 minutes) - human embryo, or 8 x proteinase K (100 µl in 250 ml RNase buffer, 37°C, 30 minutes) - formalin tissues. Subsequent rinsing in 0.5 x SSC and dehydration were performed as described above.

10 C. Prehybridization

The slides were laid out in a plastic box lined with Box buffer (4 x SSC, 50% formamide) - saturated filter paper. The tissue was covered with 50 µl of hybridization buffer (3.75g Dextran Sulfate + 6 ml SQ H₂O), vortexed and heated in the microwave for 2 minutes with the cap loosened. After cooling on ice, 18.75 ml formamide, 3.75 ml 20 x SSC and 9 ml SQ H₂O were added, the tissue was vortexed well, and incubated at 15 42°C for 1-4 hours.

D. Hybridization

1.0 x 10⁶ cpm probe and 1.0 µl tRNA (50 mg/ml stock) per slide were heated at 95°C for 3 minutes. The slides were cooled on ice, and 48 µl hybridization buffer were added per slide. After vortexing, 50 µl ³³P mix were added to 50 µl prehybridization on slide. The slides were incubated overnight at 55°C.

20 E. Washes

Washing was done 2 x 10 minutes with 2xSSC, EDTA at room temperature (400 ml 20 x SSC + 16 ml 0.25M EDTA, V_f=4L), followed by RNaseA treatment at 37°C for 30 minutes (500 µl of 10 mg/ml in 250 ml RNase buffer = 20 µg/ml). The slides were washed 2 x 10 minutes with 2 x SSC, EDTA at room temperature. The stringency wash conditions were as follows: 2 hours at 55°C, 0.1 x SSC, EDTA (20 ml 20 x SSC + 16 ml EDTA, V_f=4L).

25 F. Oligonucleotides

In situ analysis was performed on a variety of DNA sequences disclosed herein. The oligonucleotides employed for these analyses were derived from the nucleotide sequences disclosed herein and generally range from about 40 to 55 nucleotides in length.

30 G. Results

In situ analysis was performed on a variety of DNA sequences disclosed herein. The results from these analyses are as follows.

(1) DNA29101-1122 (PRO200)

35 Fetal: Lower limb expression in developing lower limb bones at the edge of the cartilagenous anlage (i.e. around the outside edge); in developing tendons, in vascular smooth muscle and in cells embracing developing skeletal muscle myocytes and myotubes. Expression also observed at the epiphyseal growth plate. Lymph node expression in marginal sinus of developing lymph nodes. Thymus expression in the subcapsular

region of the thymic cortex, possibly representing either the subcapsular epithelial cells or the proliferating, double negative, thymocytes that are found in this region. Spleen is negative. Trachea expression in smooth muscle. Brain (cerebral cortex) focal expression in cortical neurones. Spinal cord negative. Small intestine expression in smooth muscle. Thyroid - generalized expression over thyroid epithelium. Adrenal is negative. Liver expression in ductal plate cells. Stomach expression in mural smooth muscle. Fetal skin expression in basal layer of squamous epithelium. Placenta expression in interstitial cells in trophoblastic villi. Cord expression in wall of arteries and vein.

Comments: Expression pattern suggests that PRO200 may be involved in cell differentiation/proliferation.

High expression was observed at the following additional sites: Chimp ovary - granulosa cells of maturing follicles, lower intensity signal observed over thecal cells. Chimp parathyroid - high expression over chief cells. Human fetal testis - moderate expression over stromal cells surrounding developing tubules. Human fetal lung - high expression over chondrocytes in developing bronchial tree, and low level expression over branching bronchial epithelium. Specific expression was not observed over the renal cell, gastric and colonic carcinomas. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma and chondrosarcoma. Acetaminophen induced liver injury and hepatic cirrhosis.

(2) DNA30867-1335 (PRO218)

Low level expression over numerous epithelia including fetal small intestine, fetal thyroid, chimp gastric epithelium. Expression also seen over malignant cells in a renal cell carcinoma. Expression in fetal brain, over cortex. The distribution does not suggest an obvious function. Human fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult human tissues examined: kidney (normal and end-stage), bladder, adrenal, spleen, lymph node, pancreas, lung, skin, eye (inc. retina), colon, bladder, liver (normal, cirrhotic, acute failure), heart, clear cell carcinoma of kidney, gastric adenocarcinoma, colorectal carcinoma. Non-human primate tissues examined: Chimp tissues: salivary gland, stomach, thyroid, parathyroid, tongue, thymus, ovary, lymph node, peripheral nerve. Rhesus Monkey tissues: cerebral cortex, hippocampus, cerebellum, penis.

(3) DNA40021-1154 (PRO285)

Low levels of expression observed in the placenta and over hematopoietic cells in the mouse fetal liver. No expression was detected in either human fetal, adult or chimp lymph node and no expression was detected in human fetal or human adult spleen. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen,

thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), brain infarct (human), cerebritis (human), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetaminophen induced liver injury and hepatic cirrhosis.

5

(4) DNA39523-1192 (PRO273)

Expression over epithelium of mouse embryo skin as well as over basal epithelium and dermis of human fetal skin. Basal epithelial pegs of the squamous mucosa of the chimp tongue are also positive. Expression over a subset of cells in developing glomeruli of fetal kidney, adult renal tubules, and over "thyroidized" epithelium in end-stage renal disease, low expression in a renal cell carcinoma, probably over the epithelial cells. Low level expression over stromal cells in fetal lung. Expression over stromal cells in the apical portion of gastric glands. High expression in the lamina propria of the fetal small intestinal villi, normal colonic mucosa and over stromal cells in a colonic carcinoma. Strong expression over benign connective tissue cells in the hyalinized stroma of a sarcoma. Expression over stromal cells in the placental villi and the splenic red pulp. In the brain, expression over cortical neurones. Connective tissue surrounding developing bones and over nerve sheath cells in the fetus. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), eye, stomach, gastric carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetaminophen induced liver injury and hepatic cirrhosis.

Expression was present in many cells in the outer layers (I and II) of the monkey cerebral cortex. A small subset of cells in the deeper cortical layers also expressed mRNA for this chemokine homolog. Scattered cells within the molecular layers of the hippocampus and bordering the inner edge of the dentate gyrus contained chemokine homolog mRNA. No expression was detected within the cerebellar cortex. Chemokine homolog expression is not observed in infarcted brain, where cell death has occurred in the regions where the chemokine homolog normally is expressed. This probe could possibly serve as a marker of a subset of neurons of outer layers of the cerebral cortex and could possibly reveal neuronal migration disorders. Abnormal neuronal migration is a possible cause of some seizure disorders and schizophrenia. In order to gain a better appreciation of the distribution of this mRNA we will test whether the probe will cross-hybridize with mouse brain tissue.

Also shows intriguing and specific patterns of hybridization within postnatal day (P)10 and adult mouse brains. In one sagittal section of P10 mouse brain, strong signal was observed scattered within the molecular layer of the hippocampus and inner edges of the dentate gyrus. Cells in the presubiculum were moderately labeled; the signal extended in a strong band through outer layers of the retrosplenial cortex to the occipital cortex, where the signal diminished to background levels. A small set of positive neurons were detected in deeper regions of P10 motor cortex; neurons in outer layers of P10 cortex did not exhibit signal above background levels. Moderate hybridization signal was also detected in the inferior colliculus. Chemokine

homolog signal in the adult mouse brain was evaluated in three coronal sections at different levels. Strong signal was detected in the septum and in scattered neurons in the pontine nuclei and motor root of the trigeminal nerve; moderate signal was seen in the molecular layers of the hippocampus and outer layers of the retrosplenial cortex.

(5) DNA39979-1213 (PRO296)

5 Widespread expression in fetal in adult tissues. Expressed in a variety of fetal and adult epithelia, skeletal and cardiac muscle, developing (including retina) and adult CNS, thymic epithelium, placental villi, hepatocytes in cirrhotic and acetaminophen induced toxicity. Highly expressed in hypertrophic chondrocytes in developing skeletal system. The overall expression pattern, while not completely overlapping (not expressed in glomeruli, more widely expressed in CNS), is not dissimilar to VEGF. A possible role in angiogenesis should
10 therefore be considered. Human fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, great vessels, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb. Adult human tissues examined: kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure). Non-human primate tissues examined: Chimp tissues: adrenal. Rhesus Monkey tissues: cerebral
15 cortex, hippocampus, cerebellum.

(6) DNA52594-1270 (PRO868)

Expression over neuronal cells in fetal dorsal root ganglia, spinal cord, developing enteric neurons, cortical neurons. Low level expression also seen in placental trophoblast. In adult tissues the only site where
20 notable expression was observed was the normal adult prostate; as such it may represent a possible prostate cell surface receptor target antigen. Studies to further characterize the expression in adult tissues seem warranted. Low level expression also observed in a liposarcoma. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult human tissues
25 examined: liver, kidney, adrenal, myocardium, aorta, spleen, lung, skin, chondrosarcoma, etc, stomach, gastric carcinoma, colon, colonic carcinoma, renal cell carcinoma, prostate, bladder mucosa and gall bladder. Acetaminophen induced liver injury and hepatic cirrhosis. Rhesus tissues examined: cerebral cortex (rm), hippocampus(rm), cerebellum. Chimp tissues examined: thyroid, parathyroid, ovary, nerve, tongue, thymus, adrenal, gastric mucosa and salivary gland. WIG-1(WISP-1), WIG-2 (WISP-2) and WIG-5 (WISP-3) expression
30 in human breast carcinoma and normal breast tissue, Wig-2 in lung carcinoma, and Wig-5 in colon carcinoma.

(7) DNA64907-1163 (PRO1330)

In human fetal tissues there was strong specific expression over arterial, venous, capillary and sinusoidal endothelium in all tissues examined, except for fetal brain. In normal adult tissues expression was
35 low to absent, but when present appeared expression was confined to the vasculature. Highest expression in adult tissues was observed regionally in vessels running within the white matter of rhesus brain - the significance of this pattern is unclear. Elevated expression observed in vasculature of many inflamed and diseased tissues,

including tumor vasculature. In some of these tissues it was unclear if expression was solely confined to vascular endothelium. In the 15 lung tumors examined no expression was seen over the malignant epithelium, however, vascular expression was observed in many of the tumors and adjacent lung tissue. Moderate, apparently non-specific background, was seen with this probe over hyalinised collagen and sites of tissue necrosis. In the absence of a sense control, however, it is not possible to be absolutely certain that all of this signal is non-specific. Some signal, also thought to be non-specific, was seen over the chimp gastric mucosa, transitional cell epithelium of human adult bladder and fetal retina.

(8) DNA49624-1279 (PRO545)

Expression of the ADAM family molecule, ADAM 12 (DNA49624-1279) observed in normal human lung, lung tumor, normal colon and colon carcinoma.

(9) DNA59294-1381 (PRO1031)

The expression of this IL17 homologue was evaluated in a panel consisting of normal adult and fetal tissues and tissues with inflammation, predominantly chronic lymphocytic inflammation. This panel is designed to specifically evaluate the expression pattern in immune mediated inflammatory disease of novel proteins that modulate T lymphocyte function (stimulatory or inhibitory). This protein when expressed as an Ig-fusion protein was immunostimulatory in a dose dependent fashion in the human mixed lymphocyte reaction (MLR); it caused a 285% and 147% increase above the baseline stimulation index when utilized at two different concentrations (1.0% and 0.1% of a 560 nM stock). Summary: expression was restricted to muscle, certain types of smooth muscle in the adult and in skeletal and smooth muscle in the human fetus. Expression in adult human was in smooth muscle of tubular organs evaluated including colon and gall bladder. There no expression in the smooth muscle of vessels or bronchi. No adult human skeletal muscle was evaluated. In fetal tissues there was moderate to high diffuse expression in skeletal muscle the axial skeleton and limbs. There was weak expression in the smooth muscle of the intestinal wall but no expression in cardiac muscle. Adult human tissues with expression: Colon. there was low level diffuse expression in the smooth muscle (tunica muscularis) in 5 specimens with chronic inflammatory bowel disease. Gall bladder: there was weak to low level expression in the smooth muscle of the gall bladder. Fetal human tissues with expression: there was moderate diffuse expression in skeletal muscle and weak to low expression in smooth muscle; there was no expression in fetal heart or any other fetal organ including liver, spleen, CNS, kidney, gut, lung. Human tissues with no expression: lung with chronic granulomatous inflammation and chronic bronchitis (5 patients), peripheral nerve, prostate, heart, placenta, liver (disease multiblock), brain (cerebrum and cerebellum), tonsil (reactive hyperplasia), peripheral lymph node, thymus.

(10) DNA45416-1251 (PRO362)

The expression of this novel protein was evaluated in a variety of human and non-human primate tissues and was found to be highly restricted. Expression was present only in alveolar macrophages in the lung and in Kupffer cells of the hepatic sinusoids. Expression in these cells was significantly increased when these distinct

cell populations were activated. Though these two subpopulations of tissue macrophages are located in different organs, they have similar biological functions. Both types of these phagocytes act as biological filters to remove material from the blood stream or airways including pathogens, senescent cells and proteins and both are capable of secreting a wide variety of important proinflammatory cytokines. In inflamed lung (7 patient samples) expression was prominent in reactive alveolar macrophage cell populations defined as large, pale often vacuolated cells present singly or in aggregates within alveoli and was weak to negative in normal, non-reactive macrophages (single scattered cells of normal size). Expression in alveolar macrophages was increased during inflammation when these cells were both increased in numbers and size (activated). Despite the presence of histocytes in areas of interstitial inflammation and peribronchial lymphoid hyperplasia in these tissues, expression was restricted to alveolar macrophages. Many of the inflamed lungs also had some degree of suppurative inflammation; expression was not present in neutrophilic granulocytes. In liver, there was strong expression in reactive/activated Kupffer cells in livers with acute centrilobular necrosis (acetaminophen toxicity) or fairly marked periportal inflammation. However there was weak or no expression in Kupffer cells in normal liver or in liver with only mild inflammation or mild to moderate lobular hyperplasia/hypertrophy. Thus, as in the lung, there was increased expression in activated/reactive cells. There was no expression of this molecule in histiocytes/macrophages present in inflamed bowel, hyperplastic/reactive tonsil or normal lymph node. The lack of expression in these tissues which all contained histiocytic inflammation or resident macrophage populations strongly supports restricted expression to the unique macrophage subset populations defined as alveolar macrophage and hepatic Kupffer cells. Spleen or bone marrow was not available for evaluation. Human tissues evaluated which had no detectable expression included: Inflammatory bowel disease (7 patient samples with moderate to severe disease), tonsil with reactive hyperplasia, peripheral lymphnode, psoriatic skin (2 patient samples with mild to moderate disease), heart, peripheral nerve. Chimp tissues evaluated which had no detectable expression included: tongue, stomach, thymus.

(11) DNA52196-1348 (PRO733)

Generalized low level signal in many tissues and in many cell types. While endothelial cell expression was observed it was not a prominent feature in either fetal, normal or diseased tissues. Human tissues: moderate expression over fetal liver (mainly hepatocytes), lung, skin, adrenal and heart. Fetal spleen, small intestine, brain and eye are negative. Adult normal kidney, bladder epithelium, lung, adrenal, pancreas, skin - all negative. Expression in adult human liver (normal and diseased), renal tubules in end-stage renal disease, adipose tissue, sarcoma, colon, renal cell carcinoma, hepatocellular carcinoma, squamous cell carcinoma. Non human primate tissues: chimp salivary gland, vessels, stomach, tongue, peripheral nerve, thymus, lymph node, thyroid and parathyroid. Rhesus spinal cord negative, cortical and hippocampal neurones positive.

EXAMPLE 143: Isolation of cDNA Clones Encoding a Human PRO4993

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA85042. In some cases, the DNA85042 consensus sequence derives from an intermediate consensus DNA sequence which was extended using repeated

cycles of BLAST and phrap to extend that intermediate consensus sequence as far as possible using the sources of EST sequences discussed above. Based on the DNA85042 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO4993.

PCR primers (forward and reverse) were synthesized:

5 forward PCR primer 5'-AGATGTGAAGGTGCAGGTGTGCCG-3' (SEQ ID NO:619)

reverse PCR primer 5'-GAACATCAGCGCTCCCGGTAATTCC-3' (SEQ ID NO:620)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA85042 sequence which had the following nucleotide sequence

hybridization probe

10 5'-CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCC-3' (SEQ ID NO:621)

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for a full-length PRO4993 polypeptide (designated herein as DNA94832-2659 [Figure 229, SEQ ID NO:611]) and the derived protein sequence for that PRO4993 polypeptide.

15 The full length clone identified above contained a single open reading frame with an apparent translational initiation site at nucleotide positions 305-307 and a stop signal at nucleotide positions 1361-1363 (Figure 229, SEQ ID NO:611). The predicted polypeptide precursor is 352 amino acids long, has a calculated molecular weight of approximately 38,429 daltons and an estimated pI of approximately 6.84. Analysis of the full-length PRO4993 sequence shown in Figure 230 (SEQ ID NO:612) evidences the presence of a variety of
20 important polypeptide domains as shown in Figure 230, wherein the locations given for those important polypeptide domains are approximate as described above. Clone DNA94832-2659 has been deposited with ATCC on June 15, 1999 and is assigned ATCC deposit no. 240-PTA.

An analysis of the Dayhoff database (version 35.45 SwissProt 35), using the ALIGN-2 sequence alignment analysis of the full-length sequence shown in Figure 230 (SEQ ID NO:612), evidenced sequence
25 identity between the PRO4993 amino acid sequence and the following Dayhoff sequences: P_W05152; LAMP_HUMAN; P_W05157; P_W05155; I56551; OPCM_RAT; AMAL_DROME; DMU78177_1; I37246; and NCA1_HUMAN.

EXAMPLE 144: Isolation of cDNA Clones Encoding Human PRO1559, PRO725 and PRO739

30 A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above. Based upon an observed homology between this consensus sequence and an EST sequence contained within Incyte EST clone No. 4242090, Incyte EST clone No. 4242090 was purchased and its insert was obtained and sequenced. It was discovered that the insert sequence encoded a full-length protein designated herein as PRO1559 (Figure 232; SEQ ID NO:614). The DNA sequence of the insert (DNA68886) is shown in Figure
35 231 (SEQ ID NO:613).

A cDNA sequence isolated in the amylase screen described in Example 2 above is herein designated DNA43301. The DNA43301 sequence was then compared to a variety of expressed sequence tag (EST)

databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA45458. Based on the DNA45458 consensus sequence, oligonucleotide probes were generated and used to screen a human fetal brain (LIB153) library prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

PCR primers (forward and reverse) were synthesized:

forward PCR primer (45458.f1) 5'-CCAAACTCACCCAGTGAGTGTGAGC-3' (SEQ ID NO:619)

reverse PCR primer (45458.r1) 5'-TGGGAAATCAGGAATGGTGTCTCC-3' (SEQ ID NO:620)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA45458 sequence which had the following nucleotide sequence

hybridization probe (45458.p1)

5'-CTTGTTTTACCATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCC-3' (SEQ ID NO:621)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO725 gene using the probe oligonucleotide and one of the PCR primers.

A full length clone was identified that contained a single open reading frame with an apparent translational initiation site at nucleotide positions 161-163 and ending at the stop codon found at nucleotide positions 455-457 (Figure 233; SEQ ID NO:615). The predicted polypeptide precursor is 98 amino acids long, has a calculated molecular weight of approximately 11,081 daltons and an estimated pI of approximately 6.68. Analysis of the full-length PRO725 sequence shown in Figure 234 (SEQ ID NO:616) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 20, a potential N-glycosylation site from about amino acid 72 to about amino acid 75 and a tyrosine kinase phosphorylation site from about amino acid 63 to about amino acid 70. Clone DNA52758-1399 has been deposited with ATCC on April 14, 1998 and is assigned ATCC deposit no. 209773.

Analysis of the amino acid sequence of the full-length PRO725 polypeptide suggests that it possesses no significant sequence similarity to any known protein. However, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced some degree of homology between the PRO725 amino acid sequence and the following Dayhoff sequences, POL_BLVAU, PSSP_RAT, CELC36C5_7, AF019234_1, I48862, P_R12498, P_P10125, P_R26861, A64527 and P_W20495.

DNA52756, as shown in Figure 235 (SEQ ID NO:617) and which encodes native PRO739 polypeptide (Figure 236; SEQ ID NO:618) was obtained from GenBank.

EXAMPLE 145: Identification of Receptor/Ligand Interactions

In this assay, various PRO polypeptides are tested for ability to bind to a panel of potential receptor molecules for the purpose of identifying receptor/ligand interactions. The identification of a ligand for a known receptor, a receptor for a known ligand or a novel receptor/ligand pair is useful for a variety of indications including, for example, targeting bioactive molecules (linked to the ligand or receptor) to a cell known to express the receptor or ligand, use of the receptor or ligand as a reagent to detect the presence of the ligand or receptor in a composition suspected of containing the same, wherein the composition may comprise cells suspected of expressing the ligand or receptor, modulating the growth of or another biological or immunological activity of a cell known to express or respond to the receptor or ligand, modulating the immune response of cells or toward cells that express the receptor or ligand, allowing the preparation of agonists, antagonists and/or antibodies directed against the receptor or ligand which will modulate the growth of or a biological or immunological activity of a cell expressing the receptor or ligand, and various other indications which will be readily apparent to the ordinarily skilled artisan.

The assay is performed as follows. A PRO polypeptide of the present invention suspected of being a ligand for a receptor is expressed as a fusion protein containing the Fc domain of human IgG (an immunoadhesin). Receptor-ligand binding is detected by allowing interaction of the immunoadhesin polypeptide with cells (e.g. Cos cells) expressing candidate PRO polypeptide receptors and visualization of bound immunoadhesin with fluorescent reagents directed toward the Fc fusion domain and examination by microscope. Cells expressing candidate receptors are produced by transient transfection, in parallel, of defined subsets of a library of cDNA expression vectors encoding PRO polypeptides that may function as receptor molecules. Cells are then incubated for 1 hour in the presence of the PRO polypeptide immunoadhesin being tested for possible receptor binding. The cells are then washed and fixed with paraformaldehyde. The cells are then incubated with fluorescent conjugated antibody directed against the Fc portion of the PRO polypeptide immunoadhesin (e.g. FITC conjugated goat anti-human-Fc antibody). The cells are then washed again and examined by microscope. A positive interaction is judged by the presence of fluorescent labeling of cells transfected with cDNA encoding a particular PRO polypeptide receptor or pool of receptors and an absence of similar fluorescent labeling of similarly prepared cells that have been transfected with other cDNA or pools of cDNA. If a defined pool of cDNA expression vectors is judged to be positive for interaction with a PRO polypeptide immunoadhesin, the individual cDNA species that comprise the pool are tested individually (the pool is "broken down") to determine the specific cDNA that encodes a receptor able to interact with the PRO polypeptide immunoadhesin.

In another embodiment of this assay, an epitope-tagged potential ligand PRO polypeptide (e.g. 8 histidine "His" tag) is allowed to interact with a panel of potential receptor PRO polypeptide molecules that have been expressed as fusions with the Fc domain of human IgG (immunoadhesins). Following a 1 hour co-incubation with the epitope tagged PRO polypeptide, the candidate receptors are each immunoprecipitated with protein A beads and the beads are washed. Potential ligand interaction is determined by western blot analysis of the immunoprecipitated complexes with antibody directed towards the epitope tag. An interaction is judged to occur if a band of the anticipated molecular weight of the epitope tagged protein is observed in the western blot analysis with a candidate receptor, but is not observed to occur with the other members of the panel

of potential receptors.

Using these assays, the following receptor/ligand interactions have been herein identified: PRO337 binds to PRO4993, PRO1559 binds to PRO725, PRO1559 binds to PRO700 and PRO1559 binds to PRO739.

Deposit of Material

- 5 The following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA39987-1184	ATCC 209786	April 21, 1998
	DNA40625-1189	ATCC 209788	April 21, 1998
10	DNA23318-1211	ATCC 209787	April 21, 1998
	DNA39979-1213	ATCC 209789	April 21, 1998
	DNA40594-1233	ATCC 209617	February 5, 1998
	DNA45416-1251	ATCC 209620	February 5, 1998
	DNA45419-1252	ATCC 209616	February 5, 1998
15	DNA52594-1270	ATCC 209679	March 17, 1998
	DNA45234-1277	ATCC 209654	March 5, 1998
	DNA49624-1279	ATCC 209655	March 5, 1998
	DNA48309-1280	ATCC 209656	March 5, 1998
	DNA46776-1284	ATCC 209721	March 31, 1998
20	DNA50980-1286	ATCC 209717	March 31, 1998
	DNA50913-1287	ATCC 209716	March 31, 1998
	DNA50914-1289	ATCC 209722	March 31, 1998
	DNA48296-1292	ATCC 209668	March 11, 1998
	DNA32284-1307	ATCC 209670	March 11, 1998
25	DNA36343-1310	ATCC 209718	March 31, 1998
	DNA40571-1315	ATCC 209784	April 21, 1998
	DNA41386-1316	ATCC 209703	March 26, 1998
	DNA44194-1317	ATCC 209808	April 28, 1998
	DNA45415-1318	ATCC 209810	April 28, 1998
30	DNA44189-1322	ATCC 209699	March 26, 1998
	DNA48304-1323	ATCC 209811	April 28, 1998
	DNA49152-1324	ATCC 209813	April 28, 1998
	DNA49646-1327	ATCC 209705	March 26, 1998
	DNA49631-1328	ATCC 209806	April 28, 1998
35	DNA49645-1347	ATCC 209809	April 28, 1998
	DNA45493-1349	ATCC 209805	April 28, 1998
	DNA48227-1350	ATCC 209812	April 28, 1998
	DNA41404-1352	ATCC 209844	May 6, 1998
	DNA44196-1353	ATCC 209847	May 6, 1998
40	DNA52187-1354	ATCC 209845	May 6, 1998
	DNA48328-1355	ATCC 209843	May 6, 1998
	DNA56352-1358	ATCC 209846	May 6, 1998
	DNA53971-1359	ATCC 209750	April 7, 1998
	DNA50919-1361	ATCC 209848	May 6, 1998
45	DNA44179-1362	ATCC 209851	May 6, 1998
	DNA54002-1367	ATCC 209754	April 7, 1998
	DNA53906-1368	ATCC 209747	April 7, 1998
	DNA52185-1370	ATCC 209861	May 14, 1998
	DNA53977-1371	ATCC 209862	May 14, 1998
50	DNA57253-1382	ATCC 209867	May 14, 1998
	DNA58847-1383	ATCC 209879	May 20, 1998
	DNA58747-1384	ATCC 209868	May 14, 1998

	DNA57689-1385	ATCC 209869	May 14, 1998
	DNA23330-1390	ATCC 209775	April 14, 1998
	DNA26847-1395	ATCC 209772	April 14, 1998
	DNA53974-1401	ATCC 209774	April 14, 1998
	DNA57039-1402	ATCC 209777	April 14, 1998
5	DNA57033-1403	ATCC 209905	May 27, 1998
	DNA34353-1428	ATCC 209855	May 12, 1998
	DNA45417-1432	ATCC 209910	May 27, 1998
	DNA39523-1192	ATCC 209424	October 31, 1997
	DNA44205-1285	ATCC 209720	March 31, 1998
10	DNA50911-1288	ATCC 209714	March 31, 1998
	DNA48329-1290	ATCC 209785	April 21, 1998
	DNA48306-1291	ATCC 209911	May 27, 1998
	DNA48336-1309	ATCC 209669	March 11, 1998
	DNA44184-1319	ATCC 209704	March 26, 1998
15	DNA48314-1320	ATCC 209702	March 26, 1998
	DNA48333-1321	ATCC 209701	March 26, 1998
	DNA50920-1325	ATCC 209700	March 26, 1998
	DNA50988-1326	ATCC 209814	April 28, 1998
	DNA48331-1329	ATCC 209715	March 31, 1998
20	DNA30867-1335	ATCC 209807	April 28, 1998
	DNA55737-1345	ATCC 209753	April 7, 1998
	DNA49829-1346	ATCC 209749	April 7, 1998
	DNA52196-1348	ATCC 209748	April 7, 1998
	DNA56965-1356	ATCC 209842	May 6, 1998
25	DNA56405-1357	ATCC 209849	May 6, 1998
	DNA57530-1375	ATCC 209880	May 20, 1998
	DNA56439-1376	ATCC 209864	May 14, 1998
	DNA56409-1377	ATCC 209882	May 20, 1998
	DNA56112-1379	ATCC 209883	May 20, 1998
30	DNA56045-1380	ATCC 209865	May 14, 1998
	DNA59294-1381	ATCC 209866	May 14, 1998
	DNA56433-1406	ATCC 209857	May 12, 1998
	DNA53912-1457	ATCC 209870	May 14, 1998
	DNA50921-1458	ATCC 209859	May 12, 1998
35	DNA29101-1122	ATCC 209653	March 5, 1998
	DNA40021-1154	ATCC 209389	October 17, 1997
	DNA42663-1154	ATCC 209386	October 17, 1997
	DNA30943-1-1163-1	ATCC 209791	April 21, 1998
	DNA64907-1163-1	ATCC 203242	September 9, 1998
40	DNA64908-1163-1	ATCC 203243	September 9, 1998
	DNA39975-1210	ATCC 209783	April 21, 1998
	DNA43316-1237	ATCC 209487	November 21, 1997
	DNA55800-1263	ATCC 209680	March 17, 1998
	DNA94832-2659	240-PTA	June 15, 1999
45	DNA52758-1399	ATCC 209773	April 14, 1998

These deposit were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny

to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

5 The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

10 The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition
15 to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) and Figure 236 (SEQ ID NO:618).

30

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:6), Figure 8 (SEQ ID NO:18), Figure 10 (SEQ ID NO:27), Figure 14 (SEQ ID NO:35), Figure 19 (SEQ ID NO:44), Figure 21 (SEQ ID NO:51), Figure 23 (SEQ ID NO:58), Figure 25 (SEQ ID NO:63), Figure 27 (SEQ ID NO:68), Figure 29 (SEQ ID NO:73), Figure 32 (SEQ ID NO:84), Figure 34 (SEQ ID NO:89), Figure 36 (SEQ ID NO:96), Figure 38 (SEQ ID NO:101), Figure 40 (SEQ ID NO:108), Figure 42 (SEQ ID NO:113), Figure 44 (SEQ ID NO:118), Figure 46 (SEQ ID NO:123), Figure 48 (SEQ ID NO:131), Figure 50 (SEQ ID

35

NO:136), Figure 52 (SEQ ID NO:144), Figure 54 (SEQ ID NO:149), Figure 58 (SEQ ID NO:156), Figure 60 (SEQ ID NO:161), Figure 62 (SEQ ID NO:168), Figure 65 (SEQ ID NO:177), Figure 67 (SEQ ID NO:182), Figure 69 (SEQ ID NO:189), Figure 72 (SEQ ID NO:195), Figure 74 (SEQ ID NO:205), Figure 76 (SEQ ID NO:210), Figure 78 (SEQ ID NO:215), Figure 80 (SEQ ID NO:220), Figure 82 (SEQ ID NO:225), Figure 84 (SEQ ID NO:230), Figure 86 (SEQ ID NO:235), Figure 88 (SEQ ID NO:244), Figure 90 (SEQ ID NO:253),
 5 Figure 92 (SEQ ID NO:258), Figure 94 (SEQ ID NO:263), Figure 97 (SEQ ID NO:269), Figure 108 (SEQ ID NO:283), Figure 117 (SEQ ID NO:295), Figure 119 (SEQ ID NO:300), Figure 121 (SEQ ID NO:302), Figure 124 (SEQ ID NO:308), Figure 128 (SEQ ID NO:321), Figure 131 (SEQ ID NO:329), Figure 135 (SEQ ID NO:336), Figure 138 (SEQ ID NO:345), Figure 141 (SEQ ID NO:351), Figure 144 (SEQ ID NO:357), Figure 146 (SEQ ID NO:362), Figure 148 (SEQ ID NO:369), Figure 150 (SEQ ID NO:374), Figure 152 (SEQ ID
 10 NO:379), Figure 154 (SEQ ID NO:384), Figure 156 (SEQ ID NO:389), Figure 158 (SEQ ID NO:394), Figure 160 (SEQ ID NO:399), Figure 162 (SEQ ID NO:404), Figure 164 (SEQ ID NO:409), Figure 166 (SEQ ID NO:414), Figure 168 (SEQ ID NO:419), Figure 170 (SEQ ID NO:424), Figure 172 (SEQ ID NO:429), Figure 176 (SEQ ID NO:436), Figure 178 (SEQ ID NO:441), Figure 180 (SEQ ID NO:446), Figure 182 (SEQ ID NO:451), Figure 184 (SEQ ID NO:453), Figure 186 (SEQ ID NO:455), Figure 189 (SEQ ID NO:458), Figure
 15 191 (SEQ ID NO:463), Figure 193 (SEQ ID NO:465), Figure 195 (SEQ ID NO:467), Figure 197 (SEQ ID NO:469), Figure 199 (SEQ ID NO:471), Figure 201 (SEQ ID NO:476), Figure 203 (SEQ ID NO:482), Figure 206 (SEQ ID NO:487), Figure 208 (SEQ ID NO:495), Figure 210 (SEQ ID NO:497), Figure 212 (SEQ ID NO:505), Figure 214 (SEQ ID NO:507), Figure 216 (SEQ ID NO:509), Figure 218 (SEQ ID NO:514), Figure 221 (SEQ ID NO:522), Figure 224 (SEQ ID NO:525), Figure 229 (SEQ ID NO:611), Figure 231 (SEQ ID
 20 NO:613), Figure 233 (SEQ ID NO:615) and Figure 235 (SEQ ID NO:617).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure
 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:6), Figure 8 (SEQ ID NO:18), Figure 10 (SEQ ID NO:27), Figure
 25 14 (SEQ ID NO:35), Figure 19 (SEQ ID NO:44), Figure 21 (SEQ ID NO:51), Figure 23 (SEQ ID NO:58), Figure 25 (SEQ ID NO:63), Figure 27 (SEQ ID NO:68), Figure 29 (SEQ ID NO:73), Figure 32 (SEQ ID NO:84), Figure 34 (SEQ ID NO:89), Figure 36 (SEQ ID NO:96), Figure 38 (SEQ ID NO:101), Figure 40 (SEQ ID NO:108), Figure 42 (SEQ ID NO:113), Figure 44 (SEQ ID NO:118), Figure 46 (SEQ ID NO:123), Figure 48 (SEQ ID NO:131), Figure 50 (SEQ ID NO:136), Figure 52 (SEQ ID NO:144), Figure 54 (SEQ ID
 30 NO:149), Figure 58 (SEQ ID NO:156), Figure 60 (SEQ ID NO:161), Figure 62 (SEQ ID NO:168), Figure 65 (SEQ ID NO:177), Figure 67 (SEQ ID NO:182), Figure 69 (SEQ ID NO:189), Figure 72 (SEQ ID NO:195), Figure 74 (SEQ ID NO:205), Figure 76 (SEQ ID NO:210), Figure 78 (SEQ ID NO:215), Figure 80 (SEQ ID NO:220), Figure 82 (SEQ ID NO:225), Figure 84 (SEQ ID NO:230), Figure 86 (SEQ ID NO:235), Figure 88 (SEQ ID NO:244), Figure 90 (SEQ ID NO:253), Figure 92 (SEQ ID NO:258), Figure 94 (SEQ ID NO:263),
 35 Figure 97 (SEQ ID NO:269), Figure 108 (SEQ ID NO:283), Figure 117 (SEQ ID NO:295), Figure 119 (SEQ ID NO:300), Figure 121 (SEQ ID NO:302), Figure 124 (SEQ ID NO:308), Figure 128 (SEQ ID NO:321), Figure 131 (SEQ ID NO:329), Figure 135 (SEQ ID NO:336), Figure 138 (SEQ ID NO:345), Figure 141 (SEQ

ID NO:351), Figure 144 (SEQ ID NO:357), Figure 146 (SEQ ID NO:362), Figure 148 (SEQ ID NO:369), Figure 150 (SEQ ID NO:374), Figure 152 (SEQ ID NO:379), Figure 154 (SEQ ID NO:384), Figure 156 (SEQ ID NO:389), Figure 158 (SEQ ID NO:394), Figure 160 (SEQ ID NO:399), Figure 162 (SEQ ID NO:404), Figure 164 (SEQ ID NO:409), Figure 166 (SEQ ID NO:414), Figure 168 (SEQ ID NO:419), Figure 170 (SEQ ID NO:424), Figure 172 (SEQ ID NO:429), Figure 176 (SEQ ID NO:436), Figure 178 (SEQ ID NO:441),
 5 Figure 180 (SEQ ID NO:446), Figure 182 (SEQ ID NO:451), Figure 184 (SEQ ID NO:453), Figure 186 (SEQ ID NO:455), Figure 189 (SEQ ID NO:458), Figure 191 (SEQ ID NO:463), Figure 193 (SEQ ID NO:465), Figure 195 (SEQ ID NO:467), Figure 197 (SEQ ID NO:469), Figure 199 (SEQ ID NO:471), Figure 201 (SEQ ID NO:476), Figure 203 (SEQ ID NO:482), Figure 206 (SEQ ID NO:487), Figure 208 (SEQ ID NO:495), Figure 210 (SEQ ID NO:497), Figure 212 (SEQ ID NO:505), Figure 214 (SEQ ID NO:507), Figure 216 (SEQ ID NO:509), Figure 218 (SEQ ID NO:514), Figure 221 (SEQ ID NO:522), Figure 224 (SEQ ID NO:525),
 10 Figure 229 (SEQ ID NO:611), Figure 231 (SEQ ID NO:613), Figure 233 (SEQ ID NO:615) and Figure 235 (SEQ ID NO:617).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding
 15 sequence of the DNA deposited under ATCC accession number ATCC 209791, ATCC 209786, ATCC 209788, ATCC 209787, ATCC 209789, ATCC 209617, ATCC 209620, ATCC 209616, ATCC 209679, ATCC 209654, ATCC 209655, ATCC 209656, ATCC 209721, ATCC 209717, ATCC 209716, ATCC 209722, ATCC 209668, ATCC 209670, ATCC 209718, ATCC 209784, ATCC 209703, ATCC 209808, ATCC 209810, ATCC 209699, ATCC 209811, ATCC 209813, ATCC 209705, ATCC 209806, ATCC 209809, ATCC 209805, ATCC 209812,
 20 ATCC 209844, ATCC 209847, ATCC 209845, ATCC 209843, ATCC 209846, ATCC 209750, ATCC 209848, ATCC 209851, ATCC 209754, ATCC 209747, ATCC 209861, ATCC 209862, ATCC 209867, ATCC 209879, ATCC 209868, ATCC 209869, ATCC 209775, ATCC 209772, ATCC 209774, ATCC 209777, ATCC 209905, ATCC 209855, ATCC 209910, ATCC 209424, ATCC 209720, ATCC 209714, ATCC 209785, ATCC 209911, ATCC 209669, ATCC 209704, ATCC 209702, ATCC 209701, ATCC 209700, ATCC 209814, ATCC 209715,
 25 ATCC 209807, ATCC 209753, ATCC 209749, ATCC 209748, ATCC 209842, ATCC 209849, ATCC 209880, ATCC 209864, ATCC 209882, ATCC 209883, ATCC 209865, ATCC 209866, ATCC 209857, ATCC 209870, ATCC 209859, ATCC 209653, ATCC 209389, ATCC 209386, ATCC 203242, ATCC 203243, ATCC 209783, ATCC 209487, ATCC 209680, 240-PTA or ATCC 209773.

30 5. A vector comprising the nucleic acid of any one of Claims 1 to 4.

6. The vector of Claim 5 operably linked to control sequences recognized by a host cell transformed with the vector.

35 7. A host cell comprising the vector of Claim 5.

8. The host cell of Claim 7, wherein said cell is a CHO cell.

9. The host cell of Claim 7, wherein said cell is an *E. coli*.
10. The host cell of Claim 7, wherein said cell is a yeast cell.
11. A process for producing a PRO polypeptides comprising culturing the host cell of Claim 7
5 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.
12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2),
10 Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132),
15 Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270),
20 Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375),
25 Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612),
30 Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) and Figure 236 (SEQ ID NO:618).

13. An isolated polypeptide scoring at least 80% positives when compared to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) and Figure 236 (SEQ ID NO:618).

14. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under ATCC accession number ATCC 209791, ATCC 209786, ATCC 209788, ATCC 209787, ATCC 209789, ATCC 209617, ATCC 209620, ATCC 209616, ATCC 209679, ATCC 209654, ATCC 209655, ATCC 209656, ATCC 209721, ATCC 209717, ATCC 209716, ATCC 209722, ATCC 209668, ATCC 209670, ATCC 209718, ATCC 209784, ATCC 209703, ATCC 209808, ATCC 209810, ATCC 209699, ATCC 209811, ATCC 209813, ATCC 209705, ATCC 209806, ATCC 209809, ATCC 209805, ATCC 209812, ATCC 209844, ATCC 209847, ATCC 209845, ATCC 209843, ATCC 209846, ATCC 209750, ATCC 209848, ATCC 209851, ATCC 209754, ATCC 209747, ATCC 209861, ATCC 209862, ATCC 209867, ATCC 209879, ATCC 209868, ATCC 209869, ATCC 209775, ATCC 209772,

ATCC 209774, ATCC 209777, ATCC 209905, ATCC 209855, ATCC 209910, ATCC 209424, ATCC 209720, ATCC 209714, ATCC 209785, ATCC 209911, ATCC 209669, ATCC 209704, ATCC 209702, ATCC 209701, ATCC 209700, ATCC 209814, ATCC 209715, ATCC 209807, ATCC 209753, ATCC 209749, ATCC 209748, ATCC 209842, ATCC 209849, ATCC 209880, ATCC 209864, ATCC 209882, ATCC 209883, ATCC 209865, ATCC 209866, ATCC 209857, ATCC 209870, ATCC 209859, ATCC 209653, ATCC 209389, ATCC 209386,
5 ATCC 203242, ATCC 203243, ATCC 209783, ATCC 209487, ATCC 209680, 240-PTA or ATCC 209773.

15. A chimeric molecule comprising a polypeptide according to any one of Claims 12 to 14 fused to a heterologous amino acid sequence.

10 16. The chimeric molecule of Claim 15, wherein said heterologous amino acid sequence is an epitope tag sequence.

17. The chimeric molecule of Claim 15, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

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18. An antibody which specifically binds to a polypeptide according to any one of Claims 12 to 14.

19. The antibody of Claim 18, wherein said antibody is a monoclonal antibody, a humanized
20 antibody or a single-chain antibody.

20. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270),
35 Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ

ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447),
 5 Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150),
 20 Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID

NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), with its associated signal peptide; or

- (c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide.

21. An isolated polypeptide having at least 80% amino acid sequence identity to:

- (a) the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID

NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231),
 5 Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide;

(b) an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183),
 30 Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide;

NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), with its associated signal peptide; or

(c) an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID

NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide.

22. A method of detecting a PRO4993 polypeptide in a sample suspected of containing a PRO4993 polypeptide, said method comprising contacting said sample with a PRO337 polypeptide and determining the formation of a PRO4993/PRO337 polypeptide conjugate in said sample, wherein the formation of said conjugate
5 is indicative of the presence of a PRO4993 polypeptide in said sample.

23. The method according to Claim 22, wherein said sample comprises cells suspected of expressing said PRO4993 polypeptide.

10 24. The method according to Claim 22, wherein said PRO337 polypeptide is labeled with a detectable label.

25. The method according to Claim 22, wherein said PRO337 polypeptide is attached to a solid support.
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26. A method of detecting a PRO337 polypeptide in a sample suspected of containing a PRO337 polypeptide, said method comprising contacting said sample with a PRO4993 polypeptide and determining the formation of a PRO4993/PRO337 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO337 polypeptide in said sample.
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27. The method according to Claim 26, wherein said sample comprises cells suspected of expressing said PRO337 polypeptide.

28. The method according to Claim 26, wherein said PRO4993 polypeptide is labeled with a
25 detectable label.

29. The method according to Claim 26, wherein said PRO4993 polypeptide is attached to a solid support.

30. A method of detecting a PRO1559 polypeptide in a sample suspected of containing a PRO1559 polypeptide, said method comprising contacting said sample with a PRO725, PRO700 or PRO739 polypeptide and determining the formation of a PRO1559/PRO725, PRO700 or PRO739 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1559 polypeptide in said sample.
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31. The method according to Claim 30, wherein said sample comprises cells suspected of expressing said PRO1559 polypeptide.

32. The method according to Claim 30, wherein said PRO725, PRO700 or PRO739 polypeptide is labeled with a detectable label.

33. The method according to Claim 30, wherein said PRO725, PRO700 or PRO739 polypeptide is attached to a solid support.

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34. A method of detecting a PRO725, PRO700 or PRO739 polypeptide in a sample suspected of containing a PRO725, PRO700 or PRO739 polypeptide, said method comprising contacting said sample with a PRO1559 polypeptide and determining the formation of a PRO1559/PRO725, PRO700 or PRO739 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO725,
10 PRO700 or PRO739 polypeptide in said sample.

35. The method according to Claim 34, wherein said sample comprises cells suspected of expressing said PRO725, PRO700 or PRO739 polypeptide.

15 36. The method according to Claim 34, wherein said PRO1559 polypeptide is labeled with a detectable label.

37. The method according to Claim 34, wherein said PRO1559 polypeptide is attached to a solid support.

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38. A method of linking a bioactive molecule to a cell expressing a PRO337 polypeptide, said method comprising contacting said cell with a PRO4993 polypeptide that is bound to said bioactive molecule and allowing said PRO337 and PRO4993 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

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39. The method according to Claim 38, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

40. The method according to Claim 38, wherein said bioactive molecule causes the death of said
30 cell.

41. A method of linking a bioactive molecule to a cell expressing a PRO4993 polypeptide, said method comprising contacting said cell with a PRO337 polypeptide that is bound to said bioactive molecule and allowing said PRO4993 and PRO337 polypeptides to bind to one another, thereby linking said bioactive
35 molecules to said cell.

42. The method according to Claim 41, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

43. The method according to Claim 41, wherein said bioactive molecule causes the death of said cell.

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44. A method of linking a bioactive molecule to a cell expressing a PRO1559 polypeptide, said method comprising contacting said cell with a PRO725, PRO700 or PRO739 polypeptide that is bound to said bioactive molecule and allowing said PRO1559 and PRO725, PRO700 or PRO739 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

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45. The method according to Claim 44, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

46. The method according to Claim 44, wherein said bioactive molecule causes the death of said cell.

15

47. A method of linking a bioactive molecule to a cell expressing a PRO725, PRO700 or PRO739 polypeptide, said method comprising contacting said cell with a PRO1559 polypeptide that is bound to said bioactive molecule and allowing said PRO1559 and PRO725, PRO700 or PRO739 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

20

48. The method according to Claim 47, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

49. The method according to Claim 47, wherein said bioactive molecule causes the death of said cell.

25

50. A method of modulating at least one biological activity of a cell expressing a PRO337 polypeptide, said method comprising contacting said cell with a PRO4993 polypeptide or an anti-PRO337 antibody, whereby said PRO4993 polypeptide or said anti-PRO337 antibody binds to said PRO337 polypeptide, thereby modulating at least one biological activity of said cell.

30

51. The method according to Claim 50, wherein said cell is killed.

35

52. A method of modulating at least one biological activity of a cell expressing a PRO4993 polypeptide, said method comprising contacting said cell with a PRO337 polypeptide or an anti-PRO4993 antibody, whereby said PRO337 polypeptide or said anti-PRO4993 antibody binds to said PRO4993 polypeptide, thereby modulating at least one biological activity of said cell.

5 53. The method according to Claim 52, wherein said cell is killed.

54. A method of modulating at least one biological activity of a cell expressing a PRO1559 polypeptide, said method comprising contacting said cell with a PRO725, PRO700 or PRO739 polypeptide or an anti-PRO1559 antibody, whereby said PRO725, PRO700 or PRO739 polypeptide or said anti-PRO1559
10 antibody binds to said PRO1559 polypeptide, thereby modulating at least one biological activity of said cell.

55. The method according to Claim 54, wherein said cell is killed.

56. A method of modulating at least one biological activity of a cell expressing a PRO725, PRO700
15 or PRO739 polypeptide, said method comprising contacting said cell with a PRO1559 polypeptide or an anti-PRO725, anti-PRO700 or anti-PRO739 antibody, whereby said PRO1559 polypeptide or said anti-PRO725, anti-PRO700 or anti-PRO739 antibody binds to said PRO725, PRO700 or PRO739 polypeptide, thereby modulating at least one biological activity of said cell.

20 57. The method according to Claim 56, wherein said cell is killed.

FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTATAGGACCGCCTAC
CGCCGCAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCATCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCCTTC
CTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGG
CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTG
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCTCCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAAATGAAA
CGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT
TACAAAT

FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG
GTCAGCCACGGCGGGGACT**ATG**GTGAAATCCCCGGCGCTCACGCACTACTGGCCCCCTGATC
CGGTTCTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA
CCGGGGCATTTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGT
GTGAACAGCAAGAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGTGGCAGGGGCCATCGC
TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC
ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT
CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTGTAGCCATTTTGC
TTCACAGTCACCTGGAATGCCGGGAGCCCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC
GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTACGACATCATCCC
TGACAGAAGTGGCCCGGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCCAGTTCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGCCCCAGCTCTGTGCTGCG
GATCATCGTCTCATCGCCAGCCTCGTGGTCTTACCCTACCTGGGGGTGCACGGTGCGACCC
TGGGCGTGGGCTCCCTCCTGGCGGGCTTGTGGGAGAATCCACCATGGTTCGCCATCGCTGCG
TGCTATGTCTACCGGAAGCAGAAAAAGAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
AGAATGAAT**TAA**GGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTGTGTTTTGTTGTAAT
GAAAGAGGCCTTGATTTAAAGTTTTCTGTCAATTCTCTAGCATACTGGGTATGCTCAGACT
GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC
TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC
TCCTCCCCTGGACAATCTCCTCTTGGAAACCAAGGACTGCAGCTGTGCCATCGCGCCTCGGT
CACCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAAGAAATCAACAGG
TTAAAACTCGGCTTCCTTTGATTTGCTTCCCAGTCACATGGCCGTACAAAGAGATGGAGCCC
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG
GAGGCGGGTGGCACGCTGCAGCCCGGAGTCCCCGTTCACTGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCGGG
GGCAGCAAACCTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA
GCTGTGAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTCACAAAA
GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC
CTTTCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT
TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC
TTTTGAAGTAGATATATTACCTGGTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA
TTGAGAATGTACTACGGTACTTCCCTCCCACACCATAACGATAAAGCAAGACATTTTATAACG
ATACCAGAGTCACTATGTGGTCCCTGAAATAACGCATTTCGAAATCCATGCAGTGCAGTA
TATTTTTCTAAGTTTTGGAAAGCAGTTTTTTTCTTTAAAAAAATATAGACACGGTTCACT
AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA
TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTTCTATTTTCG
ATTTTCAATAAAATGTCTCTAATACAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYIIINKLHHVDES
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLCLGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQORISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTNTVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR
IFSFFPVPTVRAHLTGWMLTLKKTfVLAPSSVLRIIVLIASLVVLPYLGvHGATLGvGSLL
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPPTEEVTDIVEMREENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG
ACAAGAATAACCCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCGGGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTTCCTTTGCGGATCTTCTCCTTCTTCCCAGTCCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCCTTTCGGGATTTTCT
CCTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

FIGURE 7

-TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGAACTGAAGAAA
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

FIGURE 8

CCCCCGCGCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGGCGTGAGAGTCACTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCCTTCTTCTTCT
TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTTGGTTCTTTAAGTTCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA
TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT
CTACTTGCTGTGATCGCGCCGTGGCGCTGATGTTTATGTACTACTGAGCCAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTCTGCCCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCGAGCATTTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCCTTCCCCTCCTCCCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGG
CTGCTGGAGAGAGCGGGGAACCTCCACACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTGGAATTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAACAAGCCAGTGCGTGTAACAAAAA.

FIGURE 9

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRIFTFFLFLGVLVSIIMLSPGVE
SOLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW
NQRWLKGAEEDCSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVITYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTGCGAGCCCTCTGGCAGAGGGTTAACCTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTTCTCTGTAGAGCATTGTGCCTATTTCCCGAGTCTTTGCTGCCGAAGCTG
TGACTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGG
TGATATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAAGTGCAGTGTTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA
GCTGTACGGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC
CTTCAGTAATAGATAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTCTTTTCTTTTCTT
TTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTGCAAAAGATTAAAGTTGAATTTTACAGTTT

FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDAVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALS HFVIAGAVTGSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:**Signal Peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

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FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTTCATG
GCTGGCGCCGAACC

FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

FIGURE 14

GAGCCGCGCCGCGCGCGCGCCGCGCACTGCAGCCCCAGGCCCGCCCCACCCACGTCT
 GCGTTGCTGCCCCGCCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT
 CCGCCGGAGTCAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGTTTGC
 GCTTCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGT
 TAGTCTGCTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
 CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTCTGATTGCTTTAGTGGGTCTGATTGGAG
 CTGTAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATTCTGTACTTGTATTTATT
 GTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT
 GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT
 GTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC
 TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGTTTTGAGATTTGTTGG
 TGGCATTGGCCTGTTCTTCAGTTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA
 GGAACCAGAAAGACCCCCGCGCGAATCCTAGTGCAATTCCTTTGATGAGAAAACAAGGAAGAT
 TTCCTTTCGTATTATGATCTTGTTCACTTTCTGTAATTTTCTGTAAAGCTCCATTTGCCAGT
 TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGAATTATATATTTTTACT
 CTATGTTTTCTCTACATGTTTTTTCTTCCGTTGCTGAAAAATATTTGAACTTGTGGTCTC
 TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCAATTGTGCGGCACTGTCCACTGTGGCCTT
 TCTTAGCATTTTTACCTGCAGAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA
 TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC
 TGGAAAAAGAGTGGAATTTATTAAAATCAGAAAGTATGAGATCCTGTTATGTAAAGGGAAA
 TCCAAATTCCTCAATTTTTTTTTGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA
 TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACCCAATGTATTCTAGAAATAGTTAT
 GTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT
 CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT
 TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
 AAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGATATTTG
 ATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT
 GTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATTGTGTG
 GCTCTGTATATTCTGTAAAAAATTAAAGGACAGAAACCTTTCTTTGTGTATGCATGTTTGA
 ATTAAAAAGAAAGTAATGGAAG

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FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVFGGIGLFFSFTEILGVWL
TYRYRNQKDPRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

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FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

FIGURE 17

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCTTGC

FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGA TCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

FIGURE 19

CAGTCACCAATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTTCAGTGAACCCTTCCACCTGATTGTGTCTTATGACTGGCTG
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCTGAGTTGTCAGACAAAGTTGCCCTGCAGAGGTCAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGA
GGAGGCCCTGGGCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTCATCCATGATCTCACT
TAACCACCCCAATAAATCTGATTCTTTATTTCTCTTCTGTCCTGCACATATGCATAAGTA
CTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG
GGCAGTACCCACAAACGAAAAATAATCTGGCCCCAAAATGTCAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTCCAGCCTCATTCAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCCCTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCACAAAAACAGCTGTCGCCAACACCG
ACTCTGTCGTTGCCTTGATCTTGAACTTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGG
TTGTTTGTAGCCTAA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

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FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTTGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC
TGGCAGCGGTATGGCTTCACGGTGGCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTTCTCCTCCCATCAGTTATATTGGTATAAGCAACAGACTAATAACCAGGAACCCATC
AAAGTAGCAACCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAAGCAACATCTACAGTGAAGCAGTCTTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAGTGTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTCTGGAAGACATCCCAA
CAAGAGCATGTATACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT
CCCTGCCCTCAATTTTGTATTACTGGCAGGAATGTGGAGGAAGGGGGGTGTGGCCACAGACCC
AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATCGCCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAGTGTCTGTAAAAATGCCCCATTAGGC
CAGGATCTGCTGACATAATTGCCTAGTCAGTCTTGCCTTCTGCATGGCCTTCTTCCCTGCT
ACCTCTCTTCTGGATAGCCCAAAGTGTCCGCTACCAACACTGGAGCCGCTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGCTACTCCTCTCTAAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAAATTGAAATTGTTATTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
ATCATAACAGC

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLLGHLLTVDTYGRPILEVPESVTGPWKGDVNLPTDYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPIISYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCCGA
GGCGCCCGGGCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
GGG**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
GTGGTGATCACTTACTCCAGTCGTCACTGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
GACTACAACCACCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA
CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT
ATGTACAAAGCATCGGCATGGTGTGAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
ATTTTCCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAT
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGGCTTCCAA
ACGGTCT**TGA**ATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGACTCA
GTGAGCATTGACGGAACAGATTGAGATGAGCATTTCCTTATACAATACCAACAAGCAAA
AGGATGTAAGCTGATTTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT
TTCAAGAGGAAATGGGATGCTGTTGTAAATTTTCTATGCATTTCTGCAAACCTTATTGGATT
ATTAGTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACCTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCATCTTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCTCAAAT
CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT
TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA
CCCAACATACCATTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTCTTCTTAAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFAQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 25

GTCGTTCCCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTGCGAGGAGAGCACC CGGA
GACGCGGGCTGCAGTCGCGGGCGGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCGAGGTGCTGAGCGCCCTAG
AGCCTCCCTTGCCGCTCCCTCCTCTGCCCCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCC
GCCCCGGAGGGCGGCGGTGGATGCGGGCGCTGGGCAGAAAGCAGCCGCGATTCCAGCTGCCCGCGCGCCCCGGCG
CCCCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACC GCGCTCGCCTCCTGCAGCCGCATC
GCCCGCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCCTAGCACCACCACAGCTCAG
CCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG
ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCT
ACCTGTGCCCCCATACGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
CTGAGTCAGAACCTGGTGGTGTCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCTCTC
TCCAGCTCCACCTCACCTTCCCTGGCACAGCCATCTTTCACGCGCTGAGCACATGGAAACCCATGAAGTCCCT
TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACCTCTTCTGCCTCTGTTAGACCAAAGGTACTG
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC
CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG
CATTTTGACATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGGTGTGGTGGTGTGGT
TGCAGTATCCGGAAGCTCGAGGACTCTGAAAAAGGGGCCCCGGCAGGATCCAGTGCCATTGTGGAAGGCA
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
AGGGAGGTGTGCTGCTTCTCCAATGGGTACACAGCCGACCAGAGCGGGCTACGCAGCTCTGCAGCACTGGACC
ATCCGGGGCCCCGAGGCCAGCCTCGCCCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGAG
AAGATTGCTGGGCTGATGGAAGACACCACCCAGCTGGAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCCG
CTTAGCCCGAGCCCCATCCCCAGCCCCAAGCGAACTTGAGAATTCGCTCTCTGACGGTGGAGCCTTCCCCA
CAGGACAAGAACAAGGGCTTCTTCTGATGAGTGGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
TCCGCGCTGAGCAGGAACGGTTCCTTTATTACCAAGAAAAGAGGACACAGTGTGCGGCAGGTACGCCTGGAC
CCCTGTGACTTGACGCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG
ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTGGAATTTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGTACTGCAATTCTGGAAATTACTCA
ATTTAGTGGCAGGGTGGTTTTTTAATTTCTTCTGTTTCTGATTTTGTGTTGTTGGGGTGTGTGTGTGTTTGT
GT
TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAA
ATACCCACCACTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCTTCTTATGTATTTTCAAGATTATTCTG
TGCATTTTAAATTTACTTAACCTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT
AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTCTTAAAGATTAAAGAAATTTAAGA
CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTGTATAGTTTATATTTCATGG
CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTCACTGGACACCGTGTAGAATGCTTGATTACTTGTAC
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
GACAACTGGGGCCACCAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTGTCTTTAAAGATGTCTTG
TTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCCTTGGTCTGTGGGATTCTTCCACCAATT
ACTTTAATTAAAAATGGCTGCAACTGTAAAGACCCTTGTCTGATATATTGCAACTATGCTCCCATTTACAAATG
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGTTTGTGG
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTGTGA
AAAAA

25/237

FIGURE 26

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMEIKLPKA
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQLNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVAQAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRG
LMEDTTQLETDKLALPMSPLSPSPPIPSNKLKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLTLLDSVYSHLPDLL
```

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTGGCC
TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCAAC
TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTC
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCT
GTGGTCAAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCTTGCTCTCGCAG
TGGCCTTGGCAGGCCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTATCAC
GCCCCGTGTGGATCATCTGCTGCACACTGTGTTTATGACTTGACCTCCCCAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCACTCTGAAGAGA
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCCTGTCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCCACAG
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC
CCGTGTACCTCCTTCCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCT**GAA**
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCGGGCACCA
GTAGCAGGCCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT
GTTTTTTGTTTTTTTGGAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTGTATTTTAGTAGAGAC
AGGGTTTCACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC
ACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAACCCACCCTTTCTACTTCCAAGACTTAT
TTTCACATGTGGGGAGGTAAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT
TGTAGCATTGTTGCTTGACGTATTATTGTCTTTGATTCCAAATAATATGTTTCTTCCCT
CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLOVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSI DHLLPDDKV TALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIIITAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSHKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLISNKICNHR
DVGGGIISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSF GIGCAEVNKP G VYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

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FIGURE 29

CCCACGCGTCCGTCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTGT
GCCAGAACGGCGCGCGCGCGCACGCACGCGACACACACGGGGGGAAACTTTTTTAAAAATGAAAGGCTAGAAGA
GCTCAGCGCGCGCGCGCGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGA
CGCCCGGGCCCGGCTCGGCGCCCGCTGGGATGGTGACGCGCTCGCCGCGGGGCCGAGAGCTGCTGCACTGAAG
GCCGGCGACGATGGCAGCGCGCCGCTGCCCGTGTCCCCGCGCCGCGCCCTCCTGCTCGCCCTGGCCGGTGCTCT
GCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCAGTGCCTCTGT
TCGGAGTGGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGAATATTGCACT
ACAACGGGAAAGCAAAGAATGATCATAAATCTGGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAAC
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT
ACGGGGATATTCTGATTACGACGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATGTGTTTGAATGA
AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTTCCAGCGAAGAGCTGAAAAGCGT
CCGGGGATCATGTGGATCACATCACAACACACCAACCTCGCTGCAAAGAATGTGTTTCCACCACCCTCTCAGAC
ATGGGCAAGAGGCATAAAGAGAGAGACCCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG
AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAGAAAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAA
GTTTTACAGACCACTGAACATTCCGATCGTGTTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT
AAGTCAGGACCCATTACCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA
TGACAATGCGCAGCTTGTCACTGGGGTTTATTTCCAGGGACACCATCGGCATGGCCCCAATCATGAGCATGTG
CACGGCAGACCAGTCTGGGGGAATTTGTCATGGACCATTACAGACAATCCCTTGGTGCAGCCGTGACCTTGGCACA
TGAGCTGGGCCACAATTTCCGGATGAATCATGACACACTGGCAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCA
GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
CTGCAATGCCACCACCTGTACCTGAAGCCGGACGCTGTGTGCGCACATGGGGCTGTGCTGTGAAGACTGCCAGCT
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGGCC
TCACTGCCCAGCCCAATGTGTACCTGCACGATGGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT
CTGCCAGACTCAGGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCTTGGGATCTGCTTTGA
GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCCTTTGCCAAATGCGAGAT
GAGAGATGCTAAATGTGGAATAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCACGTGTACTTGGGCGATGA
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
AAATATTAGTGTCTTTGGGGTTCACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA
CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC
CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCCTGACCACTG
CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA
CAGTGCAAGGAAGGGCAGCGACTTCTGTGTTGAGCTTCTGTCTAAACATGGACATGCTTCAGTGCTGCTCCTGAG
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCCTTTCCCAGTGACACCTCAGCCT
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTIATTATATGAAAT
AGCAGGGTTTTAGTTTTTAAATTTATCAGAGACCCTGCCACCCATTCCATCTCCATCCAAGCAAACCTGAATGGCAA
TGAAACAACTGGAGAAGAAGTAGGAGAAAGGGCGGTGAAGTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC
AGTACTCAGGTTTGGGGTTTGCAGAAAGCCAGGGAAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGAA
TGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCCGTGCCATTACTGCATAAAATAGAGTGCATTT
GAAAT

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLDWIPVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCHYHGHVVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDKF
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFQQKCGNRVFVEEGEE
CDCGEPEECMNRCCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVGVCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN
CGKVSXSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLOQGGRIICRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRCQNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAESNRERGGQGPVGSQEHASTASLTLI

Signal peptide:

amino acids 1-28

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FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTGGGGGTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCCTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCAGTGTCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCGCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAAGTTAAT
GAAACCATAACCTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATTGTAAACCCAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA
CTTTTAACAAAAAATTTGCATCACTTTTAAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTTCGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCCTACTTGCTATCTCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT
CACGCCTGTAATCCCGGCACCTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL
LHLYH

Signal peptide:

amino acids 15-27

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FIGURE 34

GCCGCGGCGAGAGCGCGCCAGCCCCGCGCGGATGCCCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCGGC
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGCGGGCGCTGGGGCGCCCGGGCCAGG
AGGCGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGCGAGCGGCGAGGACGGACAGGACCCGACAGCAAGCACC
TGTACACGGCCGACATGTTACGCACGGGATCCAGAGCGCCGCGCACTTCGTCACTGTTCTTCGCGCCCTGGTGTG
GACACTGCCAGCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCGAGGATAACCCACCTTAA
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGCTCCTCGGGACTTCAGACACTGGAAACTGGATGC
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGGAAACCGCCAGTGCCCCCGAGCTCAAGCAAG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC
CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCGGAACTG
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTGCTCCGGAACACAGGTTCTGGCTATCCCACTC
TTCTCTGGTTCCGAGATGGGAAAAGGTGGATCAGTACAAGGGAAAGCGGGATTTGGAGTCACTGAGGGAGTACG
TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGAGACCGTCAACGCCCTCAGAGGCCCGGGTCTGGCAG
CTGAGCCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCACTTCAGAAAGGAA
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCAATTGTAAGACTCTGGCTCCTACTTGGGAGGAACCTCTCA
AAAAGGAATTCCCTGGTCTGGCGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTCCGAGGAGGGAAGAAAGTCACTGAGCACAGTGGAGGCA
GAGACCTTGACTCGTTACACCGCTTTGTCCTGAGCCAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTAC
CTCTCCTGCCCAGCTCCCGCACCTTCGCTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCACAGTGGTGGCT
GTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTTTCCAAGCCAACACACTCTACAG
ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGIACTCATGGTCACTGTGTAACATTTTCAGTGGCGATA
TATCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA
TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC
CCACGAGTTCTGGAAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCACAGTTGACTCAATAC
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC
TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC
GTGCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTCGATACTTGTCAAATCAGTTACTGTTGAGGGGAT
CCTTCTGTTTCTCAGGGGGTGAAACATGTCTTTAGTTCTCATGTTAACACGAAGCCAGAGCCACATGAACCTGT
TGGATGTCTTCTTAGAAAGGGTAGGCATGGAAAATTCACGAGGCTCATTTCTCAGTATCTCATTAACTCATTGA
AAGATTCCAGTTGTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCCTGGGTATCCAGGGAGGC
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCCTTTTAGAGG
CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTGATCTCAAGAC
CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCCATATAAACCCTTTGCATCCAACACTTTCACCCACCT
CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAAC/AGACCACTTATA
CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCAG
TATGGTTACAGATAATTCTTTTTTAAAAAAACCCAACTCCTAGAGAAGCACAACTGTCAAGAGTCTTGATACA
CACAACCTTCAGCTTGCATCAGAGTCTTGATTTCCAAGAAAATCAAAGTGGTACAATTTGTTGTTTACACTAT
GATACTTTCTAAATAAACTCTTTTTTTTTTAA

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHTGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFPKPGQEAVKYQGPRDFQTLNWMQLTLNEEPVTPEPEVEPPSAPE
LKQGLYELSASNFEHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLEYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

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FIGURE 36

CTTTTCTGAGGAACCACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAAAAA

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDGPGEEG
KHGKVGRMGPKGIKELGDMGDQGNIGKTGPIGKKGDKGEKLLGIPGEKKGAGTVCDGCRY
RKFBVGLDISIARLKTSMKFVKNVIAGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

FIGURE 38

GGTTCTATCGATTCTGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCCCGTGTGGAGTGGTGGGGCCCTGGGTGGGAATGGGCGTGT
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
CGGAAGGGAGGATCAGGGATGTTTTCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAAGTGGCCCAGCAGCGCGCCGCGC
ACACCTTTCTCATTACAGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
AGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG
GAAGCGGCGCGGAGTTTGGCCGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT
CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG
GTTCCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC
CCCTGCTGCACTGCCTCCGCGAGCTGCGGCGCGCGCGCTGGTGTGGCGCCAGAGTTTCTG
GAGTCCCTGGAGCCGGACCTGCCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG
CCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC
ACCTCTGGCACCACGGGCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCAGAGGTGAC
GGTGTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAG
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT
TTTGTGCGGCGCTTCGGGCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC
ATATCTTCCCCTTCTCCTTGATTGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCC
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG
ATGTCTTCCGGCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCCAGATTTTCTTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAAGTTGCCACCTTATGCCCG
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG
TTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC
CAGGCTGTAGGTGCCTACCTGCCCCCTACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG
CCGTTGCAGGTGTACTGGGCTGTGAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC
TTGGCCGCCATGGCCCACTTGTTTATTGCAG

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2
MGVCQRTAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL
LLLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATTVLKSFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVR LAVGSGLRPD TWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSLIRYDVTTGEP IRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGP ELAQGK
LLKD VFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

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FIGURE 40

CCTGTGTAAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATAACACTCGCTCTC
GCTTGTCCATCTCCCTCCCGGGGAGCCGGCGCGCTCCCACCTTTGCCGCACACTCCGGC
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACCTCGGATTGCAGCTCTGAACCC
CCATGGTGGTTTTTTTAAACACTTCTTTTCTTCTCTTCTCGTTTTGATTGCACCGTTTTCCA
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTGGCTTGCCATCGT
CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG
CTGGCAGAAAGGGGGTGACGCTGGGCAGCGGCGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT
CGGCTTGAGGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG
TTGCACCAATGCCTTCTTGGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC
TCCCCGCGGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC
AAGGGATTACAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG
CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC
TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC
GGAAACTGAAGATTACAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCAGGGTGTATCCG
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTCTGGGGGCTTCCCACTGTGAGGCCCTGCA
ACAATACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCCAACCTGCTCCAGCC
CTCAGATCTGCCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA
GGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC
GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA
TCACTCGGCCTGACACTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCACGGAGTTTGAGTTTGTACCA
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTGGCACTGCAGAGACTGTGCAGATTA
ATCTTGGGTTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGAATGGCCAACCTCACTTCTT
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG
CAGTAATGCAATCTGCCTCCCTTTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG
CTTCTCTTTTCTTTCAGCTATCTGTGGGGACCTTGTATTCTAGAGAGAATTCTTACTCAA
ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT
CTCACGTTGTGAGGGTTTTTTTTTCTCATTTAAAT

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADV KARS CGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGM LYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEY
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNL FIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFQGCQPKPAPALRSARSAPENFNTFRFPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGH SKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

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FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCCGCTGGTGAGTGTGCGGGGAGATTGGCAAACGCCTAGG
AAAGGACTGGGGAATAAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGCTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCAGGTGTGGGGACCGCAGGACAGACGGCCGA
TCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTGAGAGGCGCTCTGGCCACGA
AAAGTTCCTGTCCACTGTGATTCTCAATTCCTTGCTTGGTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA
ACTTTTTTCTTTTTTTTTTCTTGGTGGAAGCTGCTCTAGGGAGGGGGGAGGAGGAGGAGAAAGTGAAATGTGC
TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCCTGTCTTGGGTGCATG
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA
GGGGCTGTGCGGGGCATCCGCCTCCGCCTTCTCCACAGGCTGTGTCTGTCTGCTGGAAGATGCTAGCAATGGGG
CGCTGGCAGGATTTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTTGGGGCCAGGCCTTAGAAGAGGAGG
AAGAAGGGGCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCCACCTCCAGCCCCATCTCA
TTTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTACCACGGATCTGAGATTAAACACCTACTCTTG
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT
TTATTACTGGAAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCAACTGTTTAC
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAAAATGGCACT
TGGGTTTTTAACAGAAAAGATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG
GGGATTACTATACACTACAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGATGAAAACGACAATGCTG
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCAT
ACCCACAAAGCCTATATTTTATATACTGCCTATCAAGCTGTTCACTTCACTGCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCTGCTTAGATGAAGCAA
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTACTCTTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAAGTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTGTGCACATCACTG
ACTGGTACCCCACTCTCATTCTACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCGAGTAGATATTTTGATAACATTGACCCCTATACACCAAGGC
AAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGATGGCTTTTCAACATCACAGCCGACCCATATGA
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC
TGCAGTGCCGGTCAGGTATCCCCCAAAGACCCCAAGTAACCCTAGGCTCAATGGAGGGGTCTGGGGACCATG
GTATAAAGAGGAAACCAAGAAAAGAAGCCAAGCAAAAATCAGGCTGAGAAAAGCAAAAGAAAAGCAAAAAA
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
GGCTTGTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAACTGTCTGCTCAGTG
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG
GTGAGTCCTGAGTTCCTGCTGTGCTTCACTGCAACTGACCAAACTGCTTTGAATTATAGGAGGAGAACATA
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC

FIGURE 42B

AGTCAAAGATTGTGTACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTCAATGA
CACTTGGGTTTTTTAATTAATTCTATTTTATATATATAAATATATGTTTCTTTCTGTGAAAAGCTGTTTTCT
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC
ACAATGAATGTAACATTTTCTAAACACTTTACTAGAAGAACATTTAGTATAAAAAACCTAATTTATTTTACA
GAAAAATATTTTGTGTTTTTATAAAAAGTTATGCAAATGACTTTTATTTTATTTTCTGTACATACCATTAGAAGA
ATTTTATTTTCATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAACATCATTCAGAAAACCTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTCATGTTTGTGTCAGAGTTGAGACAACCTTTATTGTTTCTATCATAAACTATTTATGTATCTT
AATTATTTAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAATT
GTATCATTTGGTCCTAAAAATAAAAACTTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACCAACACAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATATAATAACTAA
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT
GGCACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAAACCCC
ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTATCAATGAGCATA
GATTGGTGTGGATCCTGTAGACCCTGGTGTCTTTCTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTAC
AGTATACACTTGAAGGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT
GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT
CTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGATTTTAAATTTTAAATTTTCTAGAAATATAT
GGCTCCATTTTATTTTATAGTGTAAGTTGTATTTCTTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAA
AAA

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHVMGKWHLGFNKEC
MPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTYGFYNNSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVHSPLLKNKGTVCCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIQES

Important Features:**Signal Peptide:**

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

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FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT
GGGGTCTGTCACTATGGAACATAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAT
GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTCTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA
TTGGTTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG
TGAAGGAAGTCCCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCCAAAATTAATAATGTTACCCCAAGAACCCAGGACTCC
TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAC
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTTAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCACAAGAAAGACATTGGCCGATTGAAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTCAAGTTGTATCAAGGAACTGATGC
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGTCAGTTCCTGGTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAACTTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG
TAAGATGCCTTTCTTGATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGA
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAATTCTTTGTAATAATAA

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNRNSKGVCE
ATCEPGCKFGECVGPNNKCRCPGYTGKTCSDVNECGMKPRPCQHRCVNTHGSKYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGGAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAGATATACT
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC
ATGGATAACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATAACCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC
TTTAAGACAAAACATTGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAATAATAAAG
ATTGCCATGAATCTTGCAAAA

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

Important Features:**Signal Peptide:**

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

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FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG
GACAGCGTGGCCCCGGCCCCCAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
CTGGGTCCTCACTGCTGCCCACCTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT
CAGTGGTCCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
GCAGCTCGCCCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGTATCTACAACAGCT
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGGCCCCCAGCCTG
GGGTGCAGGGCCCCCTGTGAGGGAGATTCCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA
CACTGGGTTTCAAGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
GCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT
TCCTTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
TCCTTGAGGACAGCAGGTCCCCAGGAGGAGCACCCTCCCCATGGCCCTGGGAGGCCAGGCT
GATGCACAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGTCAGAGGAGGCGGTGCTAACTG
CTGCCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
TGTGTACCAAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG
CATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
CCCCGCCAGGCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG
ACTGGCAGGTCTACTTCGCCGAGGAACAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC
AACATAAGCCAACCAACCAGCTGCTGGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
AGGCAGGCAAATGGCATTACTGCCCTGTCTCCCCACCCTGTCATGTGTGATTCCAGGCAC
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC
AGGCGTCTCAGCTTTCCTCCTCTTTACTCTTTCAGATACAATCACGCCAGCCACGTTGTTT
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTAACTTAAATAAATTGTTAC
AAAAATAAA

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FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSSGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPVTLGPRACSRHAAPGGDGSPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPE
GSCLANISQPTSC

Important features:**Signal peptide:**

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCCGGCCCCCATTCGGGCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG
CCCAGCTGTCAGCCGCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGGTGTGGCG
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTACGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT
TGGCAGGATGGGCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA
GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCACCAACCCCGTGTGTCAGCAGGATGCGCACRGCTCTGTCAACCATCACAGGG
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA
CTGACTGACCCCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCCTTGTTT
TCCAATGGCCGTGATACACTAGTGATCATGTTTACGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCCTTTC
CCCTCCTTCCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCACCACCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCCCTGGC
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTTGTAACCTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAAA

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FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDGGQGVPL
TGNVTTSQMANEQGLEFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEGSKTALQPLKHSDESKED
DGQEIA

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

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FIGURE 52

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACCTTGTCTGAAGCCCTTGTCGTAAGCCTTGAACCTACGTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTCT
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAAGATTGAAGTTCTCCAGAAGCCATTCTATCTGCCATCGCAAGACCAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGTCAGCCCATTGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGC
TCTGGGCTATGGAAAAGAAGGAAAAGGTAAATTTCCCCAGAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGGAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCTTTTAAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTATATATTTTTT
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACAGAGGAAAA
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCTGTAATCCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG
GCTGAGACAGGAGATTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

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FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLEFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL
FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDDKDGFISAREFTYKHDEL

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

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FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGA
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT
CACGGGGCTCAGTCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC
CTGCCACCCTCAACGTCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGC
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC
TGAGGAGATGTTCCCTCCAGTTCGCGATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTG
CAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCCTGAGCGGGACTCCACGGTGG
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
CCGTGATTGTGGGTGCCTCCGTGCGGGGCTTCCTGGCTGTGGTCATCTTGGTGTGCTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCCTCTCCGCCCTGTACAGTGACCTGCTGCTCG
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCCCTCTGAAACCCCG
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCCACCTGCCAGTCCCTGG
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
GGAGGGGCCGCTGTACCTGCCAGTGCTTGCCTGGCAGTGCTTCAGAGAGGACCTGGTGG
GGAGGGAGGGCTTCTCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG
TGCTCCTCCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA
AACTTGAGGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTGCTGCAG
GCTCTGCCTTCTCCATGGGGTAACCACCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTT
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAGCCTGAGGCCG
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG
CTACTCGCTCCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC
ACAGTGGCTCACGCTGTAAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT
CTGTTTGTAGTAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG
GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCCG
GGAAGCAGAGGTTGCAGTGAAGTGAAGTAGTGAAGTGGCACTGCAATTACAGCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAAA

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FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI
YNCYIMNPPDRHRGHGKIHQLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

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FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCCCTCCAG
TTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACCTGCTACATCATGAACCCCCC

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FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCCCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTGGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

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FIGURE 58

TGCGGCGACCGTCTGTACACCATGGGCCTCCACCTCCGCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT
TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGGACGTCACCCCCAGTGGTGCTGGTCC
CTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA
CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAAGTCTGCTGCTGCTGCTCATCATTGACTGCTGGATTGACAATA
TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG
GGAAGACCTTCTCACTGGAGTTCTTGACCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA
GCCTTGTTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG
AAAACGGGGCCCTACTTCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGC
TGGTTGCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGAGGCCTGGAAGGACAAGT
ATATCCGGGCCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAGACCCTGCGCGTCTGGCTTCAGGAG
ACAACAACCGGATCCAGTCACTCGGGCCCCCTGAAGATCCGGGAGCAGCAGCGGTGAGCTGTCTCCACCAGCTGGC
TGCTGCCCTACAACTACACATGGTCACTGAGAAGGTGTTCTGTCAGACACCCACAATCAACTACACACTGCGGG
ACTACCGCAAGTTCTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG
AAGCCACGATGCCACCTGGCGTGCAGCTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT
ATGAGAGCTTCCCTGACCGTGACCCATAAATCTGCTTTGGTGACGGCGATGGTACTGTGAAGTGAAGAGTGCCC
TGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAGTGTGCTGCAGGAGCTGCCAGGCAGCGAGCACATCG
AGATGCTGGCCAACGCCACCACCTGGCCTATCTGAAACGTGTGCTCCTTGGGCCCTGACTCCTGTGCCACAGGA
CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCTCTGGGGCTGTGATGGCCACGCGTTTTGCAAAGTTTGTGA
CTCACCATTCAAGGCCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCCTTTCTCT
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGGA
ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCCAGTCCCTGCCTGGGGCCATG
TGTCCCCCTATTCCTGTGGGCTTTTCATACTTGCCTACTGGGCCCTGGCCCCGAGCCTTCTATGAGGGATGTT
ACTGGGCTGTGGTCTGTACCCAGAGGTCCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCTTCCCACACACCA
GCCACAGATAGGCCTGCCACTGGTCACTGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC
TGACTGGCTTCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGAGTTTGTGCGTTCTTCGTGGTTCACAGGC
CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCAGCTCTGGATTGGGCAGCAGATGTG
CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC
CTCCCTTCAACCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTGGAGCCATGGCCTTCTGGGAACCTATGGA
GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCACCATCA
CACTGCCACCCCTGCCCTAGGCTCTCACTAGTACCAAGTGGGTGAGCACAGGGCTGAGGATGGGGCTCCTATCCAC
CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCCAGAACTTGAATGGGACCCTGAGAGAGCCAGGGGTCCCC
TGAGGCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT
CAGGGCTGCCTTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT
GGGTTCCCAAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTG
TTGCATACATGCTGGCATCTGTCTCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG
GATTCCTGGCAATAAAAGTACTCTGGATGCTGTAAAAA

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FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSVSTSWLLPYNYTWSPEKVVFVQTPTINYTLRDYRKFFQDIGFEDGWL
MQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

Important features:**Signal peptide:**

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

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FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACCTGCCA
GCCCCTCTCTTTACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCTCA
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT
GGCCTCTGGGCTGCCTCCCCTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFWLVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

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FIGURE 62

GAGCCACCTACCTTGCTCCGAGGCCAGGCCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
CCCGTGGCCGAGGCCCCCAGGTGGCTGGCGGGCAGGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG
ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCGGGGCTACCTCCGCCCTGGTGCCCTGTTTGTGCTGCTG
GCCCTGCTCGTGCTGGCTTCGGCGGGGGTGCTACTCTGGTATTTCTAGGGTACAAGCGGAGGTGATGGTCAGC
CAGGTGTACTCAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCAGGATCTTACCCGCCGGGAATCTAGTGCC
TTCCGCAGTGAAACCGCCAAAGCCCAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCTGGGAACCTTACTAC
AACTCCAGCTCCGTCTATTCCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTCATTCTCCAAATCCCCGAG
CACCGCCGGCTGATGCTGAGCCCGAGGTGGTGCAGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC
TCGGCTGCCGTCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCCTAGTGATCCTGGAAGCCAGTGTGAAA
GACATAGCTGCATTGAATCCACGCTGGGTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCCCTCCGGCTG
AAGGGGCCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACCTCCGG
CTGGAGTGGACGCTGGCAGAGTGGCGGGACCGACTGGCCATGTATGACGTGGCCGGGGCCCTGGAGAGAGGCTC
ATCACCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTGGGGGGCCATCATGGCGGTG
GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGT
GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGTCTCAGCACCCCGTACTTCCCCAGCTACTAC
TCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGATGCC
TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGACGATCCAGAACAGGAGGCTGTGT
GGCTTGGCATCTCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC
TCCGATCTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTAACCAAGTCCGACCCCTGCCCTGGA
GAGTTCCTCTGTTCTGTAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCCAACGGCCTGGAT
GAGAGAACTGCGTTTGAGAGCCACATTCCAGTGCAAAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGT
GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACC
TTCCAGTGTGAGGACCGAGCTGCGTGAAGAAGCCCAACCCGCACTGTGATGGGCGGCCGACTGCAGGGACGGC
TCGGATGAGGAGCACTGTGACTGTGGCTCCAGGGCCCTCCAGCCGCACTTGTGGTGGAGCTGTGTCTCCGAG
GGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGGTGCACACATCTGTGGGGGGGCCCTCATCGCTGACCGC
TGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGC
AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGTCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCAC
GAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACCAACCCGGTGGTGGCGCTCGGCCCGCGTGGC
CCCGTCTGCCTGCCCCGCGCTCCCACTTCTTCGAGCCCGGCCCTGCACTGCTGGATTACGGGCTGGGGCGCCTTG
CGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCACAGGACCTGTGCAGCGAG
GCCTATCGCTACCAGTGACGCCACGCTGCTGTGTGCCGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGT
GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGCCCGCTGGTTCTGGCGGGGCTGGTCAGCTGGGGCCTG
GGCTGTGGCCGGCCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG
ACCTGAGGAAGTGCCTCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAGGGCAACTGCCAAGCAGG
GGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC
CTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCCTGAGGACC
CAGGCCCCACACCCAGCCCTTCTGCCTCCCAATTCTCTCTCCTCCGTCCCTTCTCCACTGCTGCCTAATGCAAG
GCAGTGGCTCAGCAGCAAGAATGCTGGTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG
CTGTTTGGGCAGCCTTGCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCTGGTCTAACTTGGGATCTGGGAAT
GGAAGGTGCTCCCTCGGAGGGGACCTCAGAGCCCTGGAGACTGCCAGGTGGGCCTGCTGCCACTGTAAGCCAA
AAGGTGGGGAAGTCTGACTCCAGGTCCTTGCCCCACCCCTGCCTGCCACCTGGGCCCTCACAGCCAGACCT
CACTGGGAGGTGAGCTCAGCTGCCCTTGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVLRKGPDLHLASSCLWHLQGPKDLML
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSPTYFPSYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPTQGGWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDCGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDGRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAAHCFQEDSMASVT
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQQVVT

Important features:**Type II transmembrane domain:**

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512**Kringle domains.**

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

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FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTCACCGGGCCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC
CTGGAGAGTTCTCTGTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAAGTGGCCATGGCAGGCCAGCCTCCAGGTTGCGGGTGCACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGGCGCTCGGCCGCCGTGCGCCC
CGTCTGCCTGCCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGTGAAGTCAAGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCCTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

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FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTTGTTTTTTAAA
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTGGGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTCACGGAT
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAAACTCGTGTGAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGACGATGCAGATTTTG
TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTGAGATGCCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAGTGCCT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA
CAATCCAATCAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646
><subunit 1 of 1, 354 aa, 1 stop
><MW: 39362, pI: 8.35, NX(S/T): 2
MSNSVPLLCFWSLCYCFAAGSPVPFPGPEGRLEDKLHKPKATQTEVKPSVRFNLRSTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL
PLAHQLYTDVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIAKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDKPSFAFQCTDSNRFFKKGICLS
CRKNRCNSIGYNAKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:**Signal peptide:**

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

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FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCGGGCCGAGCCACCTCTTCCCCTCCCCCGC
TTCCCTGTGCGCGTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
CGGCAAAGTTTGGCCGAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACAGGCCAGACCAGGGGGCGCTCG
CTGCCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
AGAAGACTGCGGCGGCGGACGGAGAAAAACAACCTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG
CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCCGGGCCATGGAGCCCCCTGGGGAGGGCGG
CACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCGCGGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTTCGG
GCACCTCTGGACAGCCAGGATGCTGTGGCCACCCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
ACCGGATTATTTTTCCAAATCATGCTTGTGAGGACCCCGAGCAGTGTCTTAGAAGTGCAGGGCACCTTACAGA
GGCCCTGGTCCGGGACAGCCGACCTCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTACGCTCCCCTCTCCAGCCAC
TGATCTCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGCAACGTCAACATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTGCTCTCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG
AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCTGCCCTTGCAATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGTGCTGGACCCCATGATGGCCGGCGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCACCTTCA
GCAATGGCAAGGCTGCTACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGCTCTACCACACAGTTGCTTGGAGCA
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGGCTTGGGACAGACCTGTGGCTTAGGCT
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGGGACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGCTGGACCT
CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTGCGCAATTGGCAATTTCCGATGCCGGGACGAGAAGTGCCTGTGAGACAGTGGGTGGCG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTATTACAG
CTGCAGTCATTGGCAGCCTAGTGTGCGGCTGCTCCTGGTCATGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
TTCGCACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGACCCCC
CTTCTACGGGCAGCTCATTGCCCAGGGTGCCATCCACCTGTAGAAGACTTTCTACAGAGAATCCTAATGATA
ACTCAGTGCTGGGCAACCTGCCCTTCTCTGTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCCGCGCTCGTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCGCTGGGGCTTGTCCCTCGAA
CCAAACCCCGGCTCGGGCCTCTGAGGCCAGATCCAGGTACACCTTCTGCTGCTCCCTTGAGGCCCTAGATG
GTGGCACAGGTCCAGCCCGTGAAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGACCCCCACTGCCATCA
AGGCTCCCCCTCCCATCTGCTAGCACGTCTCCAGCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGACAGGCCCTGCGAGGCCGCTGTGCCCCAGCCTGGGGCCCC
CAGGACCAACCCGAGCCCCCTGGACCCACACAGCAGTCTTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG
CTCTACTGAGGCTCTCCCTGGGGCTCTACTCATAGTGGCACACCTTTTAGAGGTGGGTGAGCTCCCTCC
ACCACTTCTTCCCTGTCCCTGGATTTAGGGACTTGGTGGGCTCCCGTTGACCTATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
TCACCACCACCTGCTCCCCACGCCACCACCTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA
GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA
CCCTCCAGCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTGCCATCCCAATCCCTCCTACAGGGCCTGG
CTCACAAAAGAGTGCACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

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FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHPDRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDGVDACGDGSDGAGCSDPFPGLTPRP
VPSLPCNVTLEDFYGVFSSPGYTHLASVSHPPQSCHWLLDPHDGRRLAVRFTALDLGFGDAVH
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPDGSDGDEWDCS
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGLMRRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPFGPTRSPPGPHTAV
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

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FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAAGAAGTTTTGTAATTTTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

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FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTEFFIIAQAPEPYIVITGFEVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:**Potential type II transmembrane domain:**

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

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FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

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FIGURE 72

CAGCCCCGCGCGCCGCGGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATAACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTACAG
CCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTCCGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA
GAGGGTGGGCTTCGCAGCGAGCCCCGTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCA
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAAGTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAACTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGLAL
ALEPALASPAGAAANFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTLLR
LPQKVFD AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIIYLRDENS SR SFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEG F YVIFDRAQKRVGF AASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLV LIV LLLL PFR C
QRRPRDPEVVNDESSLVRHRWK

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

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FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGGAGCCGGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCGCGACGGCCGTGG
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGCTGGCCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCTGAAGGCATGTGCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCAGTGTGCGGGACGTCTTGACTTCAAACGCCTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTCTGGATGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC
AGAGGCCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAAGTATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGA YVLVYYNLVKAPPCGGMGNLRGRTAVVTGANS
GIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNNEVIFMALDLASLASVRAFATAFLS
SEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCR
GRLD FKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCTYAAHPGPVNSELFLRH
VPGWLRPLLRL
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARD
DRAAHLWEASKRL
AGLGPGEDAEPDED PQSEDSEAPSSLSTPHPEEPTVSQPYPSPQSSPDLSKM
THRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

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FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG
GACTCCCCGGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC
CAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCCTGAGCATGGTGCCCCAGAC
CCACACCACCTCCTGCTGATGGGACCCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACAGATGGCCAG
GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGGCCT
CGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG
TTTACTCTGGAATGTGGGCGCCCTGGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG
GCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG
ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCC
CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTTCAGCTGGAAATGTGACACTGTGAACCCGGAT
CCTGCAGAGGGCCCCAAGCCTAGACCGCGGTGTGGCTCAGCTGGAAGGTGAGTGGCCCTGCTGCGCCTGCCCAA
TCTTACACGGCCTTGTTCAGGACCAGACTGCCCGGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC
GGCTGGCAGAGCGCAGAGCTTGGAGGCCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC
CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGGAAAAAGTGCCAGTGCCCCACCTCAGGAA
GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCACACCTGCTGAAAACCAATGGCAGT
ATCCGTGGCTACAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAACTGGAGTGTAGTTGGTGAGCAG
ACCCAGCTGGAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGTGGAGCT
GGGGAGCCCACTAGACCTGTCTGCCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCAAGAACCCAGTGAGCAT
GGTCCCTGGACCCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCTGAGGTCACTGCCACCTGCGGTGTTGCACTC
TGGCTGCTGCTTCTGGGCACCGCGTGTGTATCCACCGCGCGCGAGCTAGGGTGCACCTGGGCCCAGGTCTG
TACAGATATACAGTGAGGATGCCATCCTAAACACAGGATGGATCACAGTGACTCCCAGTGGTTGGCAGACACT
TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCAGCCTCAGCAGTCCGCTGGGGGCGGATGCCGG
GACCCACTAGACTGTCTGCTCCTTGTCTCCTGGGACTCCCGAAGCCCCGGCGTGGCCCTGCTTCCAGACACC
AGCACTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCCAGGTCCCAGCT
GTCAGGGCCTCCACCCCCAGCTGGCCCCAGCTCTCCAGCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGAGG
GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCCTGCAGAGGCTTGAAGGGCCAAAAAGAAGCAGGAGCTGCAGCAT
GCCAACAGTTCCCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCTGTGAGTTAGGAAATAGAGGTTCC
AAGAACCCTTCCCAAAGCCAGGAGCTGTGCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTCCTC
AGCTCCTCAAATGAGCTGGTTACTCGTCATCTCCCTCCAGCACCCCTCTTTCTCATGAACTCCCCAACTCAG
AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC
CTTAGCCCCCTGCAGTCCCCCTAGCCCCCAGGCCCTTCCCTCTCTGGCCCCAGCCAGCTTCCAGTCCGCTGTCC
AGCTCCTCACTGTCTATCCCTGGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA
CTCAGTGAGGGTGAGGAGACTCCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCCTTCAACCCCCACCACTAT
GGGTACATCAGCGTCCCAACAGCCTCAGAGTTACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCAAGGGG
GGAGTCTTGCTGTGCCCACCTCGGCCCTGCCTCACCCCCACCCCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC
TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGTCTCCTCCGATGGCTCCTTCTCGCTGAT
GCTCACTTTGCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGCTCTAGAGCCCAGGGAGGCAGACTGC
GTCTTCATAGATGCCTCATCACTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCTGCCCCCTG
TGGGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTGAGCCACACCAGCGGCTGGGAAGGGGGATGCCTCCC
TGGCCCCCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTCGTATGCCCAAGGCTGGTGTCTCTCCT
GTAGATTACTCTGAACCGTGTCCCTGAGACTTCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAG
ACCTGGGCTGTGGTGTGTGGGTCTTGGCCTGTGTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG
TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAATTAGAGCAAAGTGACCTGGAGCCCTCAGGGAGCAA
ACATCATCTCCACCTGACTCCTAGCCACTGCTTCTCCTCTGTGCCATCCACTCCCACCACAGGTTGTTTTGGC
CTGAGGAGCAGCCCTGCCTGCTGCTTCCCCCACCATTGGATCACAGGAAGTGGAGGAGCCAGAGGTGCCTTT
GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGGAGCCCCCTCAGCCTTACCT
GGGCCCCCTCCTCTAGAGAAGAGCTCAACTCTCTCCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTG
AGGCACTGAGGCCCCACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG
TATGAGACCGTAGGTCAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT
GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
MGGMAQDSPPQILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP
DGTLLLLQPPARGHAHDGQALSTD LGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQGRHTVSGGSLLMARAEKSDEGTVMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSLCSRRLSSPRLSLAPAEA
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGPSPASSRLSSSSSLSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPRPCLTPTPSEGSLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPDYS

Important features:**Transmembrane domain:**

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

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FIGURE 78

CTCCCACGGTGTCCAGCGCCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT
CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA
ACCTCACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
TCTTTACTGATCTCTCTGTTTCGTCTTTCCAGGACCCTGCTGTCTCTCCCTCCCTTCTCCCAC
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAGCTCAGCAAACCCAGCCCC
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
GCTGAGGCCCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
AGGAACCTCTCCTCACCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCATGCAGC
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCCTGGTGCTGCTGAGCCTTCTGTGAGC
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
CGGAGACACAGAGGAACGAGAAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC
CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGGCCCTCCTGGCCAGGCCAGCAGT
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG
TCCAGCTGCCCCGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCA
GCCTGACCTAGAAGCGTTTGTCTAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
CTCATGCCCAGTGTCTGGACCCTGCCTTCTCCTCCACTCCAGACCCACCTTGTCTTCCCTCCC
TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAAGGAAGCCT
GTGAAAAACGTGATTCTTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
GACTCTGAATTTCTAACAAATGCCCAGTGAAGTCTGCGACTTGAGTTTGAAGGGCCAGTGGGCCTG
ATGAACGCTCACACCCCTTCAAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG
TCCAGGCCTTGGTTCAGGTTCAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG
TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCTTTGGAAAAAATGATGAAGA
AAACCTTGGCTCCTTCCCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
GCACAACTACTATTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT
GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCCTCCTGGGTTCAAGTGATT
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT
TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCCTGAC
CTCAAATGAGCCTCCTGCTTCAAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG
TCTGGCCCTATTTCTTTAAAAAGTGAAATTAAGAGTTGTTCAAGTATGCAAACTTGGAAG
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
TATTCGTTTTTGTGTACTTCCCTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT
TTTACAGAGCAATTATCTTGTATATACACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTTCATCA
GCTGCATAAAAAAAAAAAAAA

791237

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLQDAGEYWCGVEKRGPDSELLISLFV
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPFAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEEELGFSKEVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

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FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTACAAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

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FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCNLTNPVNPVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGPDF

Important features:**Signal peptide:**

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCTGCGTTC
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTGCTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGGAACCGGCGCTGGAAGTGTCTCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCT
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG
GAAGGCCATCCTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCTACTGGTGTGCTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATTGACCGCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA
GATACTGGTTGTATTTTTTGTCTGGTTTGGTTTTTGGGTCCTCATGTTATTTATTGCCGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT
GCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTGATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAAGTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACCAGGTCAAGGGCACCAAGGTTTCAATTCAGCCCTTACATGGACAGCTAGA
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCACCCCTAGAACCCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
TGCAGTCATGCCCCGAGTCACCTTTCACAGCGCTGTTCTCCATGAAACTGAAAAACACACAC
ACCTGCGAGA
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCTC

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FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLGKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPLVFGKVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCDNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

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FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACCTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTTCAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTGATGATGC
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACCTGCTTGACCCCGCCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTCGTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

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FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLRLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAEELGEAQAKLMEQESALR
ELRERVTOGLAEAGRGREDVRTELFRALEAVRLQNNSCEPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:**Type II transmembrane domain:**

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

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FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCCCGCAGCCCCTTCTCCTCCTTTCTCCCACGTCCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTGGCCGGCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGCTGCTCCTGCCGGGTG**ATG**GAAAACCCCAGCCCGGCCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGAGCCAGA
CGGCCTTCCCCAAGCAGTACCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCG
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG
CGCTGCAGAGCGTGACGAGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTTCGTCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCCTGCCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTCT**TAA**GACCAGAGCCCCGCAGCCCCCTGGGGCCCCCCC
GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG
TCCAGGGGCTGGCTCCACGTTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG
AGCCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFI PPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA
NNGSPCPELEEEAECVPDNCV

Important features:

Signal peptide:

amino acids 1-26

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FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA
TATTGACAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGACTCGTAGGCGGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAAATA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGAGAAATTTT
ATCCAACCTTTGTTTGGAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTTCATTCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTGAGCAGATGAACT
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT
GAGGTTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAATTTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGAGAAAGAAATC
AGTCAGCCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACCTCTTAGCAG
CAAAACAAAAAAGTAGAAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATTAAAAT
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTGTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT
TCCACAAAAA

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FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGEI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLNPFDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVNVRVSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQSDTFEIYDPRNPVNKRREESKKLMREKKERR

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

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FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCTGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTTCGCCTTGCTGACGGCGTCG
AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
GTGGCCGCGGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA
CCCTTCTGTGGGGCTCAATTTTGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG
CTCCTTCAAGTGGTTTTGGAACCGGGCTCTTGGATCTAAACCTGCCACTGGGTTCACTCTA
GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCCTCAAGTCTTTTTAGGAGTCCCTT
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCTT
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA
GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCCAGGCTGGAG
TGCAGTGGCAGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG
ATGTACGTACGACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
GAACGTGTACGCGCCGGCGCGCGCGCCCGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC
CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCCG
GAGAAAGTGGTGTGGTGTCTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCCGCCAGTCCGGC
GGGGCCATGAGCATCTCAGGACTGATGATGTCAACCCTAGCCTCGGGTCTCTCCATCGGGC
CATTTCCCAGAGTGGCACCGCGTTATTACAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
CCAAGAAGTTGCCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAC
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
TGATCCCAGATGACCCTTTGGTGTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGT
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGTGGCCACGCTACAACAAGGATGAA
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
TATGCAGGAAGGAGCCAAAGAGGGGTTTGGCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC
TGACATCCCATGATGCCCCCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT
CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC
CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGCTCAACCTGTTCTGTCTGT
TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG
TCTCTTCAATAAAGAAGTGTGATTAGAAAAAAAAAAAA

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVFFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVEYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLACNHNSTQILVNCLRALSGTKVMRVSNMKRFQLNFRDPEEIIWSMSPVVDGVVIPDD
PLVLLTQQKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:**Signal peptide:**

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

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FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
GCTGTCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA
CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
CAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC
GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAGTGTCTCCTTGGTGATCAGAGACGCGCAG
ATGCAGGATGAGTCACAGTACTTCTTTCTGGGTGGAGAGAGGAAGCTATGTGACATATAATTT
CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACC
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTTACGTGACAACAC
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACTGGAAGCCCCAAAAGGCCAGT
TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCAG
AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
GGTGAAGGCTGGGGATTGAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC
AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA
GCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA
AAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA
GGGGACAGGTTCTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCTGGAGCTGCCTCGGGTT
CAAGTGGAGCACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGT
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATCTCAACAGGAG
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGCCTGGCCCTGATCATGGAAG
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCGGGCACAGCAC
GATCCTGGATTACATCAATGTGGTCCCAGCGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
AAGCCACACCAAACAGTCCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAG
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCCAGAACCCAAATCATCCACTCAAGC
CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA
GACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC
CAATGAAGGCTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGAGGTGAGGAGTTGAGACCAGCCTG
GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG
CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA
TCTCAAAAAAAAATCCTCCAAATGGGTGGGTGTCTGTAATCCCAGCACTTGGGAGGCTA
AGGTGGGTGGATTGCTTGAGCCCAGGAGTTGAGAGACCAGCCTGGGCAACATGGTGAAACCCC
ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT
CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG
TACAAGATACAGGTATATAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAACCAACCAA
ATCCCAACCAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTCCTCACTGCTACACTCCT
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA
AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA
GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTGTCTATGGAGTAGCCATTCTTTTGTTCCTT
TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAAA

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FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPRQDWTGSTPAYGYWFK
AVTETTTKGAPVATNHQSREVEEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPENLRVMVSQANRTVLENLNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVLSLSLVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins
signature.**

amino acids 365-371

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FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGTGTATTTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA
AAGTCAAGCAGCCAGTGCGATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTGTCATCAAAGTTTCGGATATCAATGACAATGAACCAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
GATTCGCAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAA
AAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTCATTAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCCCTCCTTCCATATTATGTATTTGAAGTTTGA
AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGTTACAATC
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGATGTGCAAGTCTTAACTCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCAATTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGCTATTGATCATA
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAACAACGGAGAAAACAGATTCTATTTCTGA
GAAAAGTGAAGATTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG
GCTTTTTTACCATCAAAATTTTTTAAAGTGCTAATGTGTATTGCAACCCAATGGTAGTCTTAA
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAATAATG
TAGGAAGATATTTAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAAATTTAAAGGAGCAAAAATTTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCCTTTAT
TTAA

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FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLNNGNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVD FEHQNHYGIRAKVKNNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVDCDGSSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGS LAGSLSSLES AVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSN

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTGCGAAACATTTGACATTATT

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FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTCCTCCGCGGGG
CCCAGCCACCTTCGGGAGTCCGGGTGCCCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA
CCCCTGAGCCAGCGCGGGCCCCCGAGCGAGT**CATG**GCCAACGCGGGGCTGCAGCTGTTGGGC
TTCATTCTCGCCTTCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGAGG
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA
TGTCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCATTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCCACT
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTCC
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCCAACACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTG**TGA**CACAGAGGGCAAAAG
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACATTAGGAC
CTTAGAATTTGGGTATTGTAATCTGAAGTATGGTATTACAAACAAACAAACAAACAAAA
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCTCTCA
ATATAGGAGGGGAAGATTTTCCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAAT
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAA
ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAATATCTCTAAAT
AGGTAAATGTATTTAATTCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC
TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTCAATTCTTCATGCGTGCCCTTTT
CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT
TTGTTTTGTGTTTTATTGGTCTCTATCTCCTGAATCTAACACATTTATAGCCTACATTTTA
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACCTTTGGAGGCAAATCTTTCTGCATG
ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT
CTTGTTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT
AACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTTATATCCCCCTAACT
ACCTTTTTTGTTCCCCATTCCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA
TATCTTCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTGCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT
CACTGCCTTCCTCTCTCTACCACTTATTTCCACTGAACAAAACCTACACACATACCTTCAT
GTGGTTCAGTGCCTTCCTCTCTCTACCACTTATTTCCACTGAACAAAACCTACGCACATAC
CTTCATGTGGCTCAGTGCCTTCCTCTCTCTACCACTTATTTCCATTCTTTACGCTGTGTCT
GACATGTTTGTGCTCTGTTCCATTTTAAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG
CTATTTCACTTGAGCAAGATGATGTAATGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATG
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAAGTGCTAT
ACTAAGGGAAAGAATTGAGGAATTAAGTGCATACGTTTTGGTGTGCTTTTCAAATGTTTGA
AAATAAAAAAATGTTAAG

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FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFILAFILGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGGLWMSQSTGQI
QCKVFDSLNLSSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVNARYEFGQALFTGWAAASLCLLGALLCCSC
PRKTTSYPTPRPYPKPAPSSGKDYG

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

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FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTGACGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT
GTTCTGTCCC

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FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTA
TTTtagTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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FIGURE 101

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTTCCTGCGA

702 1237

FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCCCTGTCCC

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FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCGCCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTGTCCTGTCCTCGAA

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FIGURE 104

AGCAATGCCCTGCCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA
ATTTTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTTCTGCGAACC

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FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTTGCTGTTCTG

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FIGURE 106

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTG
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCGAGGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCCAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTTCCTGTCCCCGAAAAACAACCTCTTACCCACG

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FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACC6TTGGCATGAAGTGTATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCCTGCGAA

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FIGURE 108

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC
CGCGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCCCG
ACCGGTCCCCGCCTTTTTGTAAACTTTAAAGCGGGCGCAGCATTAAAGCTTCCCGCCCCGGT
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCCTGAGCCTCGAGCCGCGAGCACGAGCTCAAATTCCGAGGTCCCTTCACCGATGTTGT
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT
AATGTATCTGTGATGTTACAGCCTTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT
TATGGTTTCAGTCTATGTTTGGCTCCAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT
GATAAACCACATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAAG
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTCAGCATTAGC
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA
TCGTTGGTGTAAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT
AATGTATGATGACATCTCACAGGTCTTGCCCTTTAAATTACCCCTCCCTGCACACACATACAC
AGATACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC
TCTTAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT
GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGGCCACTCCCGGCCAGGCTG
CTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT
TGAATGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTCAGAGATGTTTAAATGCATA
TTTAACTTATTTAATGTATTTTCATCTCATGTTTCTTATTGTCACAAGAGTACAGTTAATGC
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA
GGAAGTGTTTTTCTGGGTGAGTAAATAACAACCTGTCATAGGGAGGGAAATTCTCAGTAGTG
ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA
CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC
TAGTTGAGAGTTTGAATGTAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCCCCAAAATTAAGAAA

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FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMQLQPFDDPNEKSKHKFMVQSMFAPTDTSDEAVWKEAKPEDLMDSKLRVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:**Transmembrane domain:**

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

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FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC
CCAAAATTAAGAATTCTTTGTCATTTTGTACATTTGCTCTATGGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTTAACTTTAAAATGAGC

FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCCAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAAATTNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

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FIGURE 113

GGTGGCCCATTCCCGGCCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTCAANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTG
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACCTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAAATGC
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

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FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACCNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTcantt
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTcatntcatgTTTTCTTATTGTCACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCCAGGCTGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTTC
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 117

GCAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCA
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAGCGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTTCACC
CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC
CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT
AACAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTGAGCATCTTGGACAAA
AGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTATGATGGAAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGTTGGTGACCAAGAGAGGGTAC
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAATCTGGCCGGGCTC
AGAGGATTGCCGAAGGGAGGCCTTCCCTTTCAGTGGACCCGGGTCAAGAATACCCACATTCCG
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCACAAAAGAAATACATGGAACCTTGGAAATCAGCCCCACGATCAAGAAAA
TGCTGGTGGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTGTCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTGAGAAGGAC
TACAACGTTGCTGTTTCGCATCACTCCCCTAAAATACGCCCAGATTTGCCTCTGGATTACGG
GAACGATGCCAATTGTGCTTACGGCTTAAAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT
GAACTCTGTCAATAGCATTTCACATTTTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAAA
TGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTTCCTTCTTAAAAATTAGACACACTTT
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC
TACTCTAAGAAGAATCTAATAGGATGCTGTTGTGTATTAAATGTGAAATTGCATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
GGGACATTTAGTTTAGTTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA
CAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTATAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG
TAATTTTAGATATGTCTTTCCTAAAAATGAATAAAATTTATGAATATGA

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FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAHCVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDSNLLYQYCDAESGSTGSGVYLRKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

7791237

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTGCGCTTGTCTTAAAGGTCCTGATCACTT
ATATCTGGAAACCAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCGTAACTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGGCCACCCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA
TGTACTTCAGTGGAAGAGTGGAAATGCATGTACCCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCCAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGTCAGAGGAGCCCTCGTAAGTTGTAAAGCACAGACTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAA

720/237

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPSCLKCQ
AKGTTLVVELAPKVLDTGRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETKTLQGTKGENSLSSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKL PVEAKLPWFKQAQEELEGA AVSEEPS

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

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FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGCTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCCGGTTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG
GCGGCGGGTCAGTCCGCGCGAGCTCCGCCAGGCCGCGGAGTGCGGGCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCCGAGTGAACCA
TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAAGTTTCTAGCTCCCAGCA
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAAGTGGCTAACATTCTTTT
TACCAGGGAAGTACCCCGCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC
AATTTGGTGTGATGGGCTTTTTTCAAAGTCCAGTAGAAGGTGCCAGACTTCCATTTATTT
GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCCAAAGCTATGGATGAATCTGTTGCAAGAAAAGTCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAAAGTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAGAATTTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT
TGGGATAAGAGAATTTTCAAGCAAGATGTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGAATAAAATTTACTGGTAC

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGTVNVTNVLHPG
IVRTNLGRHIHPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:**Signal peptide:**

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

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FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGTCAGAATTAAGTGAAGTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT
TGTGTGGAAATTATCTGCCTGGCTT

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FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCC
CTTTCCTAACCCAAACCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC
CCCAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT
TCCAAATGAAAATCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAA
ATATCATTGGATATTTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTTGAACGAGTAGCG
AATATTTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCCTCTT
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGGAGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTGG
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAACTTG
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAA

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FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTTEITSLATENIDEILNNADVALVNFYADWCRRFSQ
MLHPIFEEASDVIKEEFNENQVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMCREYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEEELTEEGLPFLILFHMKEDESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

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FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

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FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNNGGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCCTTTCCTAACCC
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTATGCTGACTGGTGTCGTTTCAGTCAG
ATGTGGCATCCAATTTTGGAGGANGCTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

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FIGURE 128

GCCCACGCGTCCGATGGCGTTACGTTGCGGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTA CTCCAGAGTACCTCAT
CCACGCTTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG
GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT
GATTACCTCTGGTGTTGACAGGTTTGAAC TTGCAC TTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTAGT
GCAATACAATAAAACTCTGAAATTAAGACTC

729/239

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:**Signal peptide:**

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

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FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCCTG
AATCCCCTTGTA TACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT
GGTCCAGTTAAGTG CATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

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FIGURE 131

CGGACGCGTGGGGGAAACCCCTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCTATCTGCAAATGAGAAATCACAAGCGCACAGGAATTTCTTGAAGATGGA
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT
TGTCCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTCTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAATTCCTCCTCATAGAGCTTTTAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGSLLWVRTQLGLPPLLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQQLTYPLHTYP
KEEELYACQRGCRFLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWSMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSYLMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLFMEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:**Signal peptide:**

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

733/237

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTGCACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGC
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

734/237

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCG
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

735/237

FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCCGGAGGT
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCCGCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCCGCGGCTG
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAAGTGTTTTAAGCCAC
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGATTTTTCTCTACTTAATAGAACTAAGGGCTTT
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTG
CATTTTGATGAGAATTCATTTTTTGCTGGGGATAAAAAAGAGCACACAACTAAAGGAGGA
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATCCATCTAACCAGACAAGA
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAC
TCAGGAACCTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC
AATGGAGGCGAAAGAGTGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

736(237)

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSSGHGEEQPPETAARQCFCQVSGYLDDCTCDVETIDRFNNYRLF
PRLQKLLESDFRYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVDPDGIKSASYKYSEEA
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLNPE
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALSKVLPFFERPDPFQLEFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTOGLGTALKILFSEKLIANMPESGPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

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FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

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FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCTGGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAATAACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTC
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

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FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW

DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGMVVS

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

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FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACCTTTATTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAAGTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

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FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
ATTGAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTCTAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTCCAGTGACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTGCTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTGTGTTGGCTTCATGCTGATCCTTGT
TGGTCCTCCGACTGTTCTGTCTGGAATAAGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
TGGTCCCTCCGACACCTTGAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
CTC**ATAG**GTTTGCAGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGAAGTGGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTCAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCACTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACCTCAAGCCCAATGCCGGTGACAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAAGTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTTGTGCTCCTTTTTTC
TGTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAAAA

742 1237

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSFVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSW
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTCEVEVQGEAIPVLALFAFVGFMILIV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

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FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGGCGAACCCTTGCGGCGCAAGGG
GTTNGCGAACCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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FIGURE 144

CCCACGCGTCCGCCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTGTTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCTCCTGGGGATCGGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGC GGCTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTCAGCGCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCT
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGC
AACAGGGACCCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA
TGGTGTCCCCCATGGTCGCTGAGACTCCCTTCGAGGATTGCACCCGCCCGTCCTAAGCCTC
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

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FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGKELRGTLTYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLFLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFSLRLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSLTPPCSE
TVTWILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

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FIGURE 146

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCGGCCAGCCTCCGCCGCCGAGCCTC
GTTCTGTCCCCGCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA
GCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC
CGCAGAGGCGGAGGCTCGCGTATTCTGTCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTGGCT
CACCTCTCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAAGAGCCTGTCTTGGAGATTTTCTGGGGAA
ATCCTGAGGTCAATTCATTATGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCACAGTGTCTGTTTCATGGCTAGA
GCAATTCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT
TTGGGAGCACACTGGGGAAGATATAGGCCCCGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTACAGGTGTTCTGGCCCTGTATGTACACATTATACA
CAGGTCGTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAAATTTGTGTCATAACATGAACATCTGGGGGCAG
ATATGGCCCCAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA
CATGGGCGGCCCTGTTCTGCTTGGCCACCTAGTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAATTTGTTTCT
TGTGAAGTAAGATTAAAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCCTGCTGGCTGTTTGGAT
AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA
AATGGTATTCAACAATTGGCAAATATCAGTCTGCTAATTCCTTCACAGTCTCTAAAGTAACAGTTCAGGCTGTG
ACTTGTGAAACAACGTGGAACAGCTCTGTCCATTTTATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCTCT
CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATGGAACTCGAGTTTATTCTGATCTGTCCAGTATC
TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
AAGACCTACATTGCTTCTTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAAATCCTCCAGGAGGAAAGGCATTC
AGAGTGTGTTGCTGTTGTGTAAGAACTGAATACTTGGAAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
ATTTTGTATAAACTGTAACATTACTGTACAGAGTACATCAACTATTTTCAGCCCCAAAAGGTGCCAAATGCATA
TAAATCTTGATAAACAAAGTCTATAAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
GTTCTACGTTTCATATATTATATGGTGTGTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAAACCTGAAAGAAACCTTATCACATTTTCCCC
AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC
TGTTAATTTAGGCATATAGAATATTAAATTCGATATTGCACCTTCTTATTTTATATAAAATAATCCTTTAATATC
CAAATGAATCTGTTAAATGTTTGATTCCCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
ATGAAAACATTCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
AAATTGAGGTACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT
GAACAAAGATGAACAAATGTATTACATTACCATTGCCACTGATTTTTTTTAAATGGTAAATGACCTTGATATAA
ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAATGTATTGTGCTTTGATACTAAA
AATCTGTAAATGTTAGTTTTGGTAATTTTTTTTCTGCTGGTGGATTTACATATTAAATTTTTTCTGCTGGTGG
TAAACATTAAATTAATCATGTTTCAAAAAAAAAAAAA

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEEDGEWWIAKQRGKRAITDNDM
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVWATSNRIGCAINLC
HNMNIWGQIWPKAVYLV CNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKEGSDRY
YPPREEETNEIERQQSQVHDTHVTRSRDDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNR
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGI
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKA FRV
FAVV

Important features:**Signal peptide:**

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

748/237

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCGCGCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCG
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGGCCGCGTGTCTCTGCTGCTGCTGGCGCTGT
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATTAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGA
CTTTGCAGATTAAAAAAGCTTCAAGAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT
TTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAA
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTGCTCCATTCTAGCTTGGGAAGC
TTCCGCTTAGAGGTCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCCCATGTAATTCTTCAATGTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT
GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCC
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA
AAAAA

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FIGURE 149

MSLLPRRAPPVSMRLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

Signal sequence:

amino acids 1-34

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FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCCGGTCTGCGTCTAGTTAACTCCAATGTCCTCCTGTG
GTTAACTGCTCTTGCCATCAAGTTTACCCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG
CAAAATCCGGGGCCTAAGAACACCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTA
TGCTCACCCTCCACTGGAGAGAGGGCGGTTTCAGCCCCCAGAACCCCCGTCCTCCTGGACTGGCATCCGAATAC
TACTCAGTTTGCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTGGTT
TACCGCCAAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTTAAACATCTACGT
GCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA
TATTCATGATCAGAACAGTAAGAAGCCCCGTCATGCTTATATCCATGGGGGATCTTACATGGAGGGCACCGGCCAA
CATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTCATCGTGATCACCATTAACTACCGTCTGGGAATACT
AGGGTTTTTAAGTACCGGTGACCAGGCAGAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG
GATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC
CTGTGTCAGCCTGTTGACCCTGTCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTAGAGCGGCACCGC
CCTGTCCAGTGGGCAGTGAACCTACCAGCCGGCCAAAGTACACTCGGATATTGGCAGACAAGGTGCGCTGCAACAT
GCTGGACACCACGGACATGGTAGAATGCCGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC
GGCCACCTACCACATAGCCTTCGGGCGGTGATCGACGGCGACGTCATCCAGACGACCCCCAGATCCTGATGGA
GCAAGGGCAGTTTCTCACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCTGAAGTTCGTGGACGGCAT
CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG
CTACCTTGAAGGGAAGACACTTTGCGGGAGACTATCAAGTTTCATGTACACAGACTGGGCCGATAAGGAAAACCC
GGAGACGCGGGGAAAACCTTGGTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCGTGGCCGCCGACCT
GCACGCGCAGTACGGCTCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAATGAAGCCAGCTG
GGCAGATTGCGCCCATGGTGATGAGGTCCCTATGTCTTCGGCATCCCCATGATCGGTCCCACCGAGCTCTTCAG
TTGTAACCTTTTCCAAGAACGACGTCATGCTCAGCGCGGTGGTCATGACCTACTGGACGAACCTTCGCCAAAACCTG
TGATCCAAATCAACCGTTTCTCAGGATACCAAGTTTCATTACACAAAACCCAAACCGCTTTGAAGAAGTGGCCTG
GTCCAAGTATAATCCCAAAGACGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC
AACGAAAGTGGCTTTCTGGTTGGAACGTTTCTCATTGTCACAACTTGAACGAGATATTCCAGTATGTTTCAAC
AACCACAAAGGTTCTCCACCAGACATGACATCATTTCCCTATGGCACCCGGCGATCTCCCGCCAAGATATGGCC
AACCACAAAGCGCCAGCAATCACTCCTGCCAACAATCCCAAACACTCTAAGGACCTCACAAAACAGGGCCTGA
GGACACAACCTGTCCTCATTGAAACCAACGAGATTATTCACCGAATTAAGTGTCAACATTGCGCTCGGGGCGTC
GCTCCTCTTCTCAACATCTTAGCTTTTGGCGGCTGTACTACAAAAGGACAAGAGGGCCCATGAGACTCACAG
GCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTCGAGAT
GAAGCAGCTGGAACACGATCAGAGTGTGAGTGCCTGCAGGCACACGACACACTGAGGCTCACCTGCCCGCCAGA
CTACACCCTCAGCTGCGCGGCTCGCCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA
CACACTGACGGGGATGCAGCCTTTGCACACTTTTAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA
CGGACATTCCACCACTAGAGTATAGCTTTTGGCCTATTTCCCTTCTATCCCTCTGCCCTACCCGCTCAGCAACAT
AGAAGAGGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGACCAGGAATGTTTTGTCCACT
GACTTAAGACAAAAATGCAAAAAGGCAGTCATCCCATCCCGGCAGACCCCTTATCGTTGGTGTTCAGTATTAC
AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTAAATAACTGCTTTAAGATCTCTACCA
CTCCAATCAATGTTTAGTGTGATAGGACATCACCATTTCAGGCCCCGGGTGTTTCCAACGTCATGGAAGCAGCT
GACACTTCTGAAACTCAGCCAAGGACACTTGATATTTTAAATTACAATGGAAGTTTAAACATTTCTTTCTGTGC
CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGGCCAGCACATGGAGCTGTAATCCAG
AGAGAAGGAAACGTAGAAATTTATTTATTAAGAATGGACTGTGCAGCGAAATCTGTACGGTCTGTGCAAGAG
GTGTTTTGCCAGCTGAACATATTTAAGAGACTTTGT

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FIGURE 151

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMPLIWFTANLDTLMTYVQDQN
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNEFVDNLYGYPEGKDTLRETIFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPSPWADSAHGDEVPIV
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPVQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPPDMS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTEISVTI AVG
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

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FIGURE 152

GGGAAAGATGCGGGCGACTCTGGGACCCCTTGGGTCTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGGTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTTCCAGTACTTGAAACGGGAGCACTCGCTGTCTGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCTTACCCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAATCCATGGACAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGGCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCCTGGTGATTCTGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC
CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCTTGAAGTTGTTTGAAGTACAGTGGAGAGAACCCAGAAAGAGGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTCTCCCTGGTGTCTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCCTGCTGCCACCACTTTTGTGACTGTACCCATGAGGTATGGAAGGAGCAGGCCTG
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC
AGAATTTTCATAGCCAGGCTGCCGTGTTGTTTGAAGTCAAGAGGCCCTTCTACTTCAGTTTTG
AATCCACAAAGAATTAATACTGGTAACACCACAGGCTTTCTGACCATCCATTCTGTTGGGT
TTGCATTTGACCCAACCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACT
TCTTCCCTGCCTTACCTTCCTTTCACTCCATTCAATTGTCTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCTATGTG
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTGTAGT
TACGATTTTGGAAATCCCACTTTGAGTGCTGAAAGTGTAAAGGAAGCTTTCTTCTTACACCTT
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT
CACTGTCAATTGAGCAGCACAGCCTGAGTGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCTCCTATGAACCTCTGTAGCCTAAATGAAAT
TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

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FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQ GALWNRVPCFLRDWELQVHFKEHGQKKN
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKL FELTVERTPEEEKLHRDVF LPSVDNMKLP EMTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQE QSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
CTGATGGTGGGTCTGTTAACTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT
TGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAAATCTGTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTGAAGAGAAATCATGCCCGACCTGTGACGGAGCCCCCTGTGA
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCGAGTGTGGCCGAGCGCAGCATGGAAGGTGATGCCC
CGCATCATTTTAAAGCTGGTCTCAGTGCATGTGTTTATTGCGCACGGAGACAGGTACCCACTGTATGTATTCCCA
AAACAAAGCGACCCAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA
TTAGTGCATGTCAAAGGATCCGGAGCCTCTTTGAAAGCCCTTGAACCTCTTGCCTCTTTACCCAAATCACC
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGCTGCTGAGGGATA
TCTATCTAAAGAAACACAAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCCTGGGAAAA
GCCGGACCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA
GGCACCAGCCAAGTGGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAAGAAACAGTATCTGGAAGAGGAGC
AGGCTCGTCACTACCTCTACGTTTAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCTGTGG
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTGAGCT
TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
GGGAAAGACGGGAGAAGAAATTGTACTTCGGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAAAACCATCG
GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT
CACCAGTTCTCAGTGCCTTGGGCCTTTGAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGGATTCTTTACATGGCGTTCGATGTACATTCCACACCT
CTTTCTGCCAAGACCACCACAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAA
GGGACATGTTTTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTACAGGGAAGGATTCTAAAAGG
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAGGTCCACTTCTAGTTTTGTCTGTTAC
TAAGGGTAGAAGATTATTGCTTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGGTTGGGTTGAACAGT
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAATGGCCAGTTCAAGAGGAATAGAAGGTACTT
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTTAATCTTAGACATT
TTTACCTTGTCTTGTAAAGAAATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTTCTGTAAAGG
GCCAGATTGTAAATATTTAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTACATACTACTCAACTCTGT
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA
GATGGTGACCAGACTTGGCCCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCCTCCAGTAACCTCTGCTAGAAACA
CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT
TTCTAAGACCAGTTTATAGTACTCTTATTCCGTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
GAGGCTAGAAGATGAATTCAGGCACCTTTCTTCCAATAAACTAATTATGGCTCATTCCTTTGACAAGCTGTAGA
ACTGGATTCATTTTAAACCATTTTCATCAGTTTCAAAATGGTAAATTTCTGATTGATTTTTAAATGCGTTTTTGG
AGAATTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
TGATTTCTGAACTAATGGTGCTAATTCAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCC
AACTTTTTCTCTTTGTTTTGTCCAGTGTTGCATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

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FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLLALAAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY
EALLYCNIPVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSHSVRILYNGVDVTFHTSF
CQDHHKRSPKPMCPLNLVRFVKRDMFVALGGSGTNYYDACHREGF

Signal sequence:

amino acids 1-18

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FIGURE 156

AAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCTTTTGAAGAACAGTACTGTGGA
GCTATTTAAGAGATAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
GCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGACGCGCCTGAAGCACAAAGCAGAT
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAACAACGGAGGAGCTCTGACTTCCCACTGTCCCATTCTAT
GGGCGAAGGAACCTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAAATGAT
TCCTGCGGACTGCACCGGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGACTCTGTGGGAGACCGG
ATGCACCCAGATACGCTATTCACTTCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACCGAGCTTTTTCGCCCT
GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG
TCAATTAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA
CGACAATGCGCCTTACTTTCTGTAAGTGAATTAGAAATAAAAATTAGTGAATATGCAGCCACTGAGATGCGGTT
CCCTCTACCCACGCCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCGAATTGGTGCTGAAACGCGCCCTGGACCG
CGAAGAAAAGGCTGCTCACCACCTGGTCTTACGGCTCCGACGGGGCGACCCGGTGCACAGGCACCGCGCG
CATCCGCGTGATGGTTCTGGATGCGAACGACAACCGACCCAGCGTTTGTCTAGCCCGAGTACCGCGCAGCGTTCC
GGAGAATCTGGCCTTGGGCACGCGAGCTGCTTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT
GAGGTATTCCTTCGGGTATGTGGACGACAAGGCGGCCAAGTTTTCAAAGTAGATTGTAATTGAGGGACAATATC
AACAATAGGGGAGTTGGACCACGAGGAGTCAAGGATCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATA
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCACCTCTCT
CGCCAGCTCGGTTCCCGAAAACCTCTCCAGAGGGACATTAAATTGCCCTTTAAATGTAAATGACCAAGATTCTGA
GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAATCTTACGGAAATTACTA
TAGTTTAGTACAGACATAGTCTTGGATAGGGAACAGGTTCTTAGCTACAACATCACAGTGACCGCCACTGACCG
GGGAACCCCGCCCTATCCACGGAAACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCGCGTCTT
CCCTCAGGCTCTTATTCGGCTTATATCCCAGAGAACAATCCCAGAGGAGTTCCCTCGTCTCTGTGACCGCCCA
CGACCCCGAGCTGTGAAGAGAACGCCAGATCACTTATTCCTGGCTGAGAACACCATCAAGGGGGCAAGCCTATC
GTCCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA
CTTGCAAGTGAAAGTGATGGCGCGGGACAACGGGCACCCGCCCTCAGCAGCAACGTGTCTGAGCCTGTTCTGT
GCTGGACCAGAACGACAATGCGCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTCCACTGGCGTGGAGCT
GGCTCCCGCTCCGACAGAGCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC
CTGGCTGTCTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG
CACGGCGCGAGCCCTGCTGGACAGAGACGGCTCAAGCAGAGCCTCGTAGTGGCGTCCAGGACACGGCCAGCC
CCCTCTCTCCGCCACTGTACGCTCACCGTGGCGGTGGCCGACAGCATCCCCAAGTCTGGCGGACCTCGGCAG
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG
CGTCTTCCITGGCCTTCGTCTCTGCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCAAGCCTGCTGCAGGC
TTAGGAGGGCGGCTTGACAGGAGCGCCGGCGTCCGACTTTGTGGGCGTGGACGGGGTGAGGCTTTCTGACAGC
CTATTCCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACTGATCTTCCCCAGCCCACTATGCAGA
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAGCGAGCCCTTTTGTCTGTCAGGTGATTCGGTATTTTCTAAAGA
CAGTCATGGGTTAATTGAGGTGAGTTTATATCAATCTTCTTTCTTTTTTTTTTAATTGCTCTGTCTCCCAAGC
TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCCTCAAACCTCCTAGGCTCAAGCAATTATCCACCTTTGCCT
CCGGTGTAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCTAT
CTATCTATCTATCTATCTATTACTTTCTTGTACAGACGGGAGTCTCACGCCTGTAATCCAGTACTTTGGGAGGC
CGAGGCGGTGGATCACCTGAGGTTGGGAGTTTGGAGACAGCCTGACCAACATGGAGAAACCCGCTCTATACTAA
AAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAAT
TGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG
AAACTCTATCTCA

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FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPEELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRFPPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELVLKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSCLASSVPENSPRGTLIALLNVI
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLIALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVD RD SGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADLGSLESPA
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLQASGGGLTGAPASHFVGVD
GVQAFLLQTSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFFNCSSVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLS
IYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLWEAEAGGSPEVGSLRPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

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FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCAAGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGAGGTGGCAACTGGGTCTT
ACAGCTGCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAAGTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT
CTGGTTC

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FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWVLTAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGSDPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

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FIGURE 160

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGGCCCGGCCTGCGCGCCCCGGCCCCG
CGCGCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCGGGCCCCGCGCCCCG
GCCCCGCGCCAGGTGAGCGCTCCGCCCGCCGCGAGGCCCGCCCCGGCCCCGCCCCGCCCCG
CCCCGGCCGGCGGGGAACCGGGCGGATTCTCGCGCGTCAAACACCTGATCCCATAAAAC
ATTTCATCCTCCCGGGCGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCCGCCGCCCTCG
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGC
GGAGCGCGCCGAGCCTCGTCCCGCGGCCCGGGCCGGGGCCGGGCCGTAGCGGCGGCGCCTGGA
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCGCCCCGAAACGACTTTTCAGTCCCCGACGCGC
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCCGCGCTACACACGCTGCACCTGGACCGC
TGCGGCCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGCCCCATGTGCACCCGCGATGCCCT
CCGTGACCTTGGCCGCGCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCGGGCACGCCACTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG
ACAGCCCGCCGGGCAACGGCTCTGGCCCACGGCACATCAATGACTCACCCCTTGGGACTCTG
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCGAGCCACT
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGAAGGCTCAGGTGCC
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGTGTGGACAGTGCT
TGGGCCCTGCTGACCCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC
GGGGTCTCTCTCCACGCCGCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG
GTCCTCCCTGATGGACGCCTGCCGCCCCGCCACCCCATCTCCACCCCATCATGTTTACAGGG
TTCGGCGGCAGCGTTTGTTCAGAACCGCGCCTCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAATAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAAA
AAAA

7611237

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRLLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAAF TGLALLEQLDLSDNAQLRSVDPA
TFHGLGRLHTLHLDRCLQELGPGFLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQNRVAHVHHPHAFRDLGRLMTLYLFANNLSALPTEALAP
LRALQYLRLNDNPWVCD CRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSEGS GALPSLTCSLTPLGLALVLWTVLGPC

Important features:**Signal peptide:**

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

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FIGURE 162

GGAAGTCCACGCGGGAGCTTGGATGCCAAAGGAGGAGGACGGCTGGGTCTCTTGGAGAGGACTAC
 TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGGACTTTAC
 AGTCCCACAGAACCCTCCTCCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA
 AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCTCTTTTGGGCTTATCTCTGGCG
 GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC
 CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTAGGGTTG
 TTTCCAGAGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT
 GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT
 GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
 ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG
 ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA
 TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACC CGCAAACGCAGTGATGGCAGGAAAT
 ACCCAGAGCTGGTGTCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA
 CTCACAGCACTGGATGGTGGCTCTCCGCCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
 CTTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG
 AGGACAGTCCGGTAGGCTTCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC
 AACGGAGAGATTTCTTACTTTTCCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT
 CAATCCCTTGACAGGAGAAATTGAACTAAAAAAACAACCTCGATTTGAAAAACTTCAGTCCT
 ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT
 CAAGTGATAGATGTGAACAGCACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT
 AACTGAGAACGCGCCTGAAACTGTGGTTGCACCTTTTCAGTGGTTTCAGATCTTGATTACAGGAG
 AAAATGGGAAAATTAGTTGCTCCATTCTAGGAGGATCTACCCTTCTCCTGAAATCCGCGGAA
 AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT
 CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
 TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTGCTC
 CGCGAGAACAACAGCCCCGCCCCGACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG
 CACCAACGCCCAGGTCACCTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCTCACAT
 CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTGCCCTCAGGTCTCTGGACTACAGG
 GCCCTGCAGGGGTTCCAGTTCGCGCTGGGCGCTTCAGACCACGGCTCCCGGCGCTGAGCAG
 CGAGGCGCTGGTGC GCGTGGTGGTGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC
 CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGGCGCCGAGCCGGGCTAC
 CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCCTGGCTGTCTGTACCA
 GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCCGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA
 CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGTGGTCAAGGAC
 AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC
 CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGACCCAGGCCCAGGCCGACTTGCTCACCG
 TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTT
 GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTTGGTGCCCGA
 GGGCCCCCTTCCAGGGCATTGTGGGACATGAGCGGCACACGAGCACTCCAGAGCTACC
 AGTATGAGGTGTCTTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCTCTGAAGCCGATT
 ATCCCCAACTTCCCTCCCAAGTGCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA
 TAACCTTTGGGTTCAATATTGAGTACCATAGTTGACTTTTACATTCCATAGGTATTTTATTT
 TGTGGCATTTCCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT
 TTACTCTTGATTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT
 CCTGGTTCTT

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FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLGLSLAGAAEPRYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLSPFEFFQAEQV
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVDVTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLLKSAENFYTLTLLTERPLDRESRAEYNITITVTDLGTPMLITQ
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFLGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAO
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

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FIGURE 164

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTG
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
TGATTCCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTACAGGACCT
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
CACTTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
TGTTCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC
GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT
GTGGTGGTAACTCAAGCCGACCAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA
CTGGTTGCTTGTATTTTCCTTATTCTTTTAAATTAGTTTTATTATGTATGCTACCATTGAA
CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAGAATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

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FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333
><subunit 1 of 1, 360 aa, 1 stop
><MW: 39885, pI: 4.79, NX(S/T): 7
MVPAAGRPPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NETLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKEPMARFNHTDRTLTLKIFIFNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296**Thioredoxin domain**

amino acids 211-227

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FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTGCGCGCGCCACGATGCTGCAGGGGCCCTGGCT
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTTA
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCCACCCGAATCTTGTAGAAATATTCAAACATAA
AAATCATGAATATTTTAA

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FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSAAGLEFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHSCLCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSEKDLKKSIVLWLDKSLQCTCE
EMNDINAPYLVMGQKQGELVITSVKRWQKGQREFKRISRSIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

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FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTTGCTCGCGATC
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTG
TATCCACCCCATTGCGGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG
ACCATCCTGGGTGCGTGGCTGAACCTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT
TGTTGGGACCCAAAACCCATTGCTTCTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCCTTGTTGGTTCCCAGAGCACCAGCGA
GCCACGGCCAACATGCTCGCCACCATGTCGAACCCTCTGGGCGTCCTTGTTGGCCAATGTGCT
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCGGTTAATGCTCGGTGTCTATACCATCC
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTG
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCCTGGGGCCAGCACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGGAGCCCCACCCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

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FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPVLV
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLEFSLACVPFALVSQLOGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEAATGMIFVLGQAEGLIMLAMTALTVRRESEPSLSTCQQGEDPLDWTVSLLL MAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

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FIGURE 170

GTCCACATCCTGCTCAACTGGGTGAGGTCCCTCTTAGACCAGCTCTTGTCATCATTGCTGAAGTGGACCAAC
TAGTTCCCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA
TGGCCTTGCTTGGGGTCTGCTGTTTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGG
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAGAAGTCTAGTGGT
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG
CTACTTATTTCTTTTAGGGGATTGTCAGGAGGTGACCCTCTCACGGTGAATACCAAGTGTGAGAGGAAGTGCC
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAAGTGGGCGGGAGGAGAGGGCGGAGGCAAGCTGGGGCCGCTT
CCAGGTGTTGTCAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTT
GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCAATGACCACCAGCCACGTTTCCCAAGGCGAGCAGGA
GCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCC
TAACACCTGACACCTACACTCTGTCTCCAGTGAGCACTTGGCTTGATGTGCTGTTGGGCGCTGTGAGAG
CAACATGCGAAGTCTAGTGGTGAAGGAGCTGGACAGGGAATCCATTTCATTTTGGATCTGGTTAACTGC
CTATGACAAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGCTTGGACTCCAATGACAAATAG
CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT
GACCGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCCTCAGTAAGCACATGCCCTCCAGAGGT
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTCGACCTCTAGACTATGAAAAGAACCC
TGCCTACGAGGTGGATGTTCAAGCAAGGACCTGGTCCCAATCCTATCCAGCCCATTCGAAAGTTCTCATCAA
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCAGCTGACATGGGCGCTCCAGCCATCACTGGTGTGAGAGC
TCTTCCCAAGGACAGTTTTATTGCTCTTGTGTCATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG
CTGGCTGAGCCAAGAGCTGGGCGCACTTCAAGGTGAAAGAAGTAAATGGCAACACATACATGTTGCTAACAATGC
CACACTGGACAGAGAGCAGTGGCCCAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
AGCCAAGAAACAGCTCAGCATTCAGATCAGTGACATCAACGACAATGCACCTGTGTTGAGAAAAGCAGGTATGA
AGTCTCCACCGCGGGAAACAACCTTACCCTCTCTTCACTCATTAACATCAAGGCTCATGATGACAGACTTGGGCAT
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCGAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA
GGTCACTGCTCAGAGGTCACTGAAGTATGAAGAGATGCCCGGCTTTGAGTTCAGGTGATCGCAGAGGACAGCGG
GCAACCCATGCTTGCTGATCCAGTGTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC
CATCGAGACTCCCAATGGCTTGGGCCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT
CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAATGGAGAGCCCTCTACAGCATCCGCAATGG
AAATGAAGCCACCTCTTCATCCTCAACCTCATAAGGGGAGCTGTTCTGTCAATGTCAACATGCCAGAGCCT
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT
GAGGGTCATGTTTGTCAACAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT
GCTGACGGTGATCTGCTGGCTGTACTGTTGGGCATCTTGGGTTGATCCTGGCTTGTTCATGTCCATCTGCCG
GACAGAAAAGAGGACAACAGGGCCTACAACCTGTGGGAGGCGGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC
CCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCTGTGCTCAGGGGTGAGGCAGGTGAGCCTTGTGAAGT
CGGGCAGTCCACAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCTGACAGCCCCCTT
CCACCTCACCCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACAGGGAGCACCGGCGGAGAGCCGAGAGGT
GCTGCAAGACAGGTCACCTCTTTTCAACCATCCCGTGAGGAGGAATGCCTCCCGGGAGAACCTGAACCTTCC
CGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCCTCTGAAGGTTGCAGGCAGCCCCACAGGGAGGCTGGC
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACCAGCCTCTCTGCAACCTGAGACGGCAGCGACATCT
CAATGGCAAAGTGTCCCCTGAGAAAGAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC
TGCCTTCGCGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTGAGCAATCTCCAGCTGCT
GTCCTTGCTGCATCAGGGCCAATTCCAGCCCCAACCAACCCAGGAAATAAGTACTTTGGCCAAGCCAGGAGG
CAGCAGGATGCAATCCACAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC
CAGCACAGGTCTGGCCCTGAGCCGGCTGAGCGCCCTGACCCGGCCTGGATGGCGAGACTCTCTTGGCCCTCAC
CACCAACTACCGTGACAATGTGATCTCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG
CAAGGCAGAGGCACAGAGCTGAGCCCAACAGGCACGAGGTGGCCAGCACCTTGTCTCGGAGATGAGCTCACT
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCGTGGAGGCCGCTCCGAGGCGCTGCGGCGGCTCTCGGT
CTGCGGGAGGACCTCAGTTTAGACTTGGCCACAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG
AAAGACGGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGGTGCTGTAACATACCTCAGACGCCT
CTGGATCCAAGAACCAGGGCCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACTCACTAGCTAG
CGGCGGCTGAGAACTTTAGGGTGACTGATGCTACCCCAACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC
TGACCAAGCAGCCCTTGAAGCAGCTCTGAGTCTTTTGGAGGACAGGACGGTTTGTGGCTGAGATAAGTGTT
TCCTGGCAAAACATATGTGGAGCACAAGGGTCAGTCTCTGCCAGAACAGATGCCACGGAGTATCACAGGCAGG
AAAGGTGGCCTTCTTGGGTAGCAGGAGTCAAGGGGCTGTACCCTGGGGGTGCCAGGAATGCTCTGACCTAT
CAATAAAGGAAAAGCAGTAAAAA

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FIGURE 171

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISESASLRTRIPDRALDPDTGPNTLHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPFAFAESS
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGPNIPIAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS
YRIQDSPVAHLVAIDSNTGEVTAQRSLNYEEMAGFEFQVIAEDSGQPMLASSVSVWVSLDDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTT
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA
GWDPCLQAPFHLTPTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLPEP
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGQFQPKPNHRGNKYLAKPGGS
RSAIPDTDGPSARAGGQTDPEQEELDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATSAASGMKVQGDPGGKTGTGEGKSRGSS
SSSRCL

```

Important features:**Signal peptide:**

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTCTCAGCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTGGTCCCAACACATT
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGTCCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAATCACTGAAGTCCTTGGGAACTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCCTGGTCAGCGCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAGGGCGCGGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

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FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDFFPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDVPTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKEFFYAISS
SKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:**Signal peptide:**

amino acids 1-23

Potential transmembrane domains:amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

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FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNGANACTATTTTTTGGATTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

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FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGTTGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTTACATTGGCTATTTTATGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCCTC

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FIGURE 176

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCTTGGGGGGCTCCGGGATTTGCTACCTTTT
TGGCTCCCTGCTCGTCAACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCTTGGCGAA
GGAGGGCGAGCCAGGCAGCCTCTTCCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTCCCTGGGCAGCAGGCGAATCGCACTGGAGGCCCTCTTGGCTTG
CCCCTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA
GGAGAACCAGTGGTTGGGAGTCACTGTTTCGGAGCCAGGGGCTTGGGGGCAAGATTGTTACCTGTGCACACCGATA
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTGGCTGCTTTGTGCTCAGCCAGGA
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCCCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG
TCCCTACGAGGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCCCTCATCCCGTCCCTGCCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAAGGTCTGGTGGCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGGCCAACCA
CAAGGGTGTGTGGTCTCCTGCGCAAGGACAGCGCCAGTGCCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCG
CCTGACCTCCGGCTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTATGGCTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGGGGGTCACTG
GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCCGGATCAGCCTGGCTGTCTGGGGGA
CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCTTTGATGGTGGTGGGAAAGTCTTCATCTACCA
TGGGAGCAGCCTGGGGGTGTGCGCAAACTTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCCTGTCAAGCAGCTTGGATATGGATGGATGGGGAACCAATACCCTGACCTGCTGGTGGGCTCCTGGCTGACAC
CGCAGTGTCTTTCAGGGCCAGACCCATCCTCCATGTCTCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT
GGAGCAGCCCCAATGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT
TCCCCGTGTGACGTTCTGAGCCGTAACTTGAAGAACCACAGCACCAGGCCCTCGGGCACCSTGTGGCTGAAGCA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAATGTCAAAGACAAGCTTCGGGCCATTGT
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC
CCCCATCTCAATGCCACCAGCCAGCACCAGCGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACC
TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCATGAGTGGGCAGCCAGTCAATGGCTGGAGCTGAT
GGTGACCAACCTGCCATCGGACCCAGCCAGCCCGAGGCTGATGGGGATGATGCCCATGAAGCCAGCTCCTGGT
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCTGCGGAGAAGCCACTCTGCCTGTCCAA
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCAT
CCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC
CCAGCAACTCTTCTTCTCTGTTGTGGTGGAGGGCGAGAGGCCATGCACTGTGAGCGGGATGTGGGCAGCAAGGT
CAAGTATGAGGTACCGTTTCCAACCAAGGCCAGTGCCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGG
GCAGAAAGGGCTTTGCTCTCCAGGCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGGCGGA
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGGCGGCAGGAGCCAGCATGTCTTGGTGGCCAGTGTCTCTGC
TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAACCTGTGTGGTGTTCAGCTGCCCACTCTA
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCGCTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGA
TGCTCCACAGTATCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGT
CATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAGATGGGATTCTT
CAAACGGGCGAAGCACCCGAGGCCACCGTGCCCACTAGCACTGCGGTGAAGATTCTCGGGAAGACCGACAGCA
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCGGGCGGGAGGGCCCGGATGCACA
CCCCATCCTGGCTGTGACGGGCATCCGAGCTGGGGCCCGATGGGCATCCAGGGCCAGGCACCGCTTAGGTTCC
CATGTCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
GGGCTGCTGGTGTGCGCATCAAGATTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAAC
TCCTCCCAACCTTCCCTTAGAGTGTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG
TGAGAAGGGCAGGGGTGTCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCCATTCACCTGT
GTAACAGGACCCCAAGGACCTGCCTCCCGGAAGTGCCTTAACTAGAGGGTCGGGGAGGAGGTTGTGTCACTGA
CTCAGGCTGCTCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCTGCCATCAGTCTAGTGGTTTCTGTGGT
TTCGTCTATTTATTAATAAATATTTGAGAACAATAAAAAAAAAAAAAAAAAAAAA

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FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGFLFACPLSLEETDCYRVDIDQGADMOKESKENQWL
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELGGGEWKFCG
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGWPDILVGAFFERQEELGGAVVYVYNQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDLNQDGFDPDIAGAPFDGDGKVFIYHGSSLGVVAKPSQVLE
GEAVGIKSFYSLSGSLDMDGNQYPDLLVGLADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQPSQRAEIHFLKQGCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN
ENASHVECELGNPMKRGAQVTFFYLILSTSGISIETTELEVELELLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKEYEVTVSNQGQSLRTLGS AFLNIM
WPHEIANGKWL LYPMQVELEGGQGPQGKGLCSRPNIHLHDVDSRDRRRRELEPPEQQEPGE
RQEPSMSWVPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDRAAVLHVWGRLWNSTFLEEY
SAVKSLEIVVRANITVKSSIKNLMLRDASTVIPVMVYLDPMVVAEGVPWWVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGS PRREGP
DAHPIAADGHPGLGPDGHPGPGTA

Important features:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-
407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408
and 1031-1047

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FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCACTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTGGGACGGCGGTAATTTTC
TGGATGATAAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCAACGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTTCAGATGGTCATACCTACTCTTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCCACCACTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTGATACCAAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAACAGACTTGATACAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC
ATGGGATCCAGAATAAATGGTGTTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAAGTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTCACGAGAACAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG
ATAATTCTAAGTGAAATTTAAATAAATAAATTTTAAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

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FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLRPERSRFDTSILPI
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPQCQTELSNIQKRQGVKLLGQYIPLCDEDEGYKPTQCHGSGVCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

Important features:**Signal peptide:**

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

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FIGURE 180

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC
CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGCGGCGACAAGATCTGGCTGCCCTTCCCGTGCTCCTTCTGGCC
GCTCTGCCTCCGGTGCTGCTGCTGCGCTGGGCGCGCGCTTACACCTTCCCTCGATAGCGACTTACCTTTACCCCTT
CCCGCCGGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCCGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTGA
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCCAAAACCTTAGTTTTGAACAAAGAAAA
TCAGATGGAGTTTCACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTTCAGCACCATT
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAGATTGGAAG
AAATATATTACTGGCACAGATATATTGGATATGAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC
AGACTAAGCAAAAGTGGGCACATACAAATCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC
AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTGAGCCATTCAAGTTTAT
ATGCTGAAGAGTCTGTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAAACTAGAGTACGTAAACATTGAAA
AATGAGGCATAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAATATTTTGAGATATA
AAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG
TTGTACTTAAGTGTGAACAGGAATATTTTGCAGAATATAGGTTAACTGAATGAAGCCATATTAATAACTGCAT
TTTCTAACTTTGAAAAATTTGCAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCAATTGCAACACC
AGTCTGTTTTTAACAGGTTCTATTACCCAGAACTTTTTGTAAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT
TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCAA
CTTTTCTCTATTACATATGCATCTCTCTATAATGTAATAGAATAATAGCTTTGAAATACAATTAGGTTTGTG
AGATTTTTATAACCAAATACATTTTCAGTGTAAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
CCAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG
AAATGAAGAATATAGTTTAAAGCTTCCCTCCATAGGGACACATTTTCTCTAACCCCTTAAGTAAAGTGTAGGA
TTTTAAATTAATGTGAGGTAAATAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
TAATCATGTTATGTTAATTTTAACATGATTGCTGACTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA
TTGCTAAAATGATCTGGGCCTACCATAAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAAACAGGAA
AGAATTTAGAAAACTTGAGAAAACCTAATCCAAATAAATTCACTTAAGTAGAACTATAAATAAATATCTAGA
ATCTGACTGGCTCATCATGACATCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
AACTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTTGAATTATTTTTGTAAGCAGGTACATTTTATA
AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATTAAAAATTTTATTATAACAACTTTTAT
TAAAATGGCCTTTTCTGAACACTTTTATTTATTGATGTTGAAGTAGGATTAGAAACATAGACTCCCAAGTTTAAAA
CACCTAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC
TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAAATTTTAAAGTTATGCCATTATAACGTTGTTTAT
GACTACATTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC
TCTTAGGCCCTTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA
AGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTGCCTGTTAAATTTGCAATGAGAAGCAAATTTACA
GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAAGATTCTA
CCTCTCCTGTATGGCTGTTACTGTACTCTCTGACTCCTTACCTAACAAATGAATTTGTACATAATCTTCT
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACCTCTTACCATATAAAAACGATAATTGCTT
TATTTGGAAAAGAAATTTAGGAATACTAAGGACAATTATTTTATAGACAAAGTAAAAAGCAGATATTTAAGAGG
CATAACCAAAAAAGCAAACTTGTAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACTGTTTATCTGCTT
CATATGCTTTTTTTAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTT
AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTC
CATAATGTAGCAGTTACCGTGTTCACTCACACTAAGGCTAGAGTTTGTCTGATATGCATTTGGATGATTAAT
GTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGGTGTGTAATTTTATGGTAAAAATTAATCCTTCTTA
CACATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAATGTATGTCTCCTCAATGAAGATTCTTTAT
GTGAAATTTTAAAGACATTGATTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTG
CTCAACTGCTTTTATACTTATAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA
AAATTATCAAAGGAAA

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FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLFPFVLLLAALPPVLLPGAAGFTPSLSDFTFTLPAGQKECFYQPMPLKASLEIEY
QVLGDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFTEL
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDN
IQESNFDVRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

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FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAAGTCCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTATGATCCTCC
TTCTTTTTCCTTTTCTTCACCTTCATTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCILLLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM

DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS

TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

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FIGURE 184

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGGCCCTCACGCTC
CTCCCCTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

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FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVDGIGQTLVPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

7861237

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGCGGCTCTCGGCGGCCACCCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACTCCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTCTCTTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAAGCATAACCCCTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPCAEEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLScriQ
KDHHQASNSSRLHTCQRH

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCCACCNGTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

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FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG
CTGGGCCGTCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGTCCGCCGCCA
GGGTTTGAGGATGGGGAGTAGCTACAGGAAGCGACCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGA
AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCT
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC
TTAAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGTTTAAATAAAGATGACTATATCAGAGACTTGAAAAG
GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG
AGTGTCCAAAACCTGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATGGCATTGAAGTTACATCCTGATAA
AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA
CTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC
TGCTGTTAATTTCTGGAGAAGTGTGTTTGTAAATTTTACTCCCCAGGCTGTTCACTGCCCAGTATTTAGCTCC
CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTTACTTGAATTTGGAGCTGTTAACTGTGGTGTATAGAAT
GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCAATTTTTCGGTCTGGAATGGCCCACTGAAATA
TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTGTCAATGCAGCATGTAGAAGTACAGTGACAGAATTTG
GACAGGAAATTTTGTCACTCCATACAACTGCTTTTGTGCTGCTATTGGCTGGCTGATCACTTTTGTTCAAA
AGGAGGAGATTTTGTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCACTCATTTGGATGCTAA
AGAAATATATTTGGAAGTAATACATAATCTCCAGATTTTGAATCTTTCGGCAACACACTAGAGGATCGTTT
GGCTCATCATCGGTGGCTGTTATTTTTCATTTTGGAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAAGT
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAATGTTTCTCTGCACCAGACATCTGTAGTAA
TCTGTATGTTTTTTCAGCCGTCTTAGCAGTATTTAAAGGACAAGGAACCAAGAATATGAAATTCATCATGGAAA
GAAGATTCTATATGATATACTTGCCCTTTGCCAAAGAAAGTGTGAATTTCTCATGTTACCACGCTTGGACCTCAA
TTTTCTGCGCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTACT
ACCGAGTTACGAAGAGCATCAAATCTTTTATGTTGAGCTTAAGTTTGGTACACTAGATTGTACAGTTTCTGA
GGGACTCTGTAACATGTATAACATTCAGGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTCATGAGTA
TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
ACCCACCACCTTCAACGAAGTATGACAAAGAAACACAACGAAGTCTGATGGTTGATTTCTATTCTCCGTG
GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAAGAATGGCCCGGACATTAACCTGGACTGATCAACGTGGG
CAGTATAGTTGCCAACAGTATCAATCTTTTGTGCCCAGGAAAACGTTCAAAGATACCCCTGAGATAAGATTTT
TCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTCCTGAGAAT
CTGGGGTCTAGGATTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTCAGTGAAAAGTCTTACAAGG
GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT
CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAGAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA
AGCTGGGATCAGGGCTATCCAAGTGTAAAGTTTATTTCTACGAAAGAGCAAAGAGAAATTTCAAGAAGAGCA
GATAAATACCAGAGATGCAAAAGCAATCGCTGCTTAAATAGTGAAGAAATTTGAAACTCTCCGAAATCAAGGCAA
GAGGAATAAGGATGAATTTGATAATGTTGAAGATGAAGAAAAGTTTAAAAGAAATTCAGACAGATGACATCAG
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTTATCTTAGACTTGCAAGTTGTACTGCCA
GAATATCTACAGCACTGGTGTAAAAGAAGGGTCTGCAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA
GACTTTGCAGGCTATAATATATGTTTACACATGAGAACAAGAAATAGAGTCATCATGATTTCTTTGTTATTTGCT
TTTAAACAACCTTTAAAAAATATTAACAGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCACTCCATG
GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
ATCTACATAAATGTCTAAGTTGTATAAAGTECCATTTCCCTTCACGTTTTTGGCTGACCTGAAAAGAGGTAAC
TAGTTTTTGGTCACTTGTTCTCTAAAAATGCTATCCCTAACCATATATTTATATTTCTTTTTAAAAACACCCAT
GATGTGGCAGTAACAAACCTGTATGCTGTATTATTTATGAGGAGATTCTTCAATGTTTTCTTTCTTCTCTCA
AAGGTTGAAAAATGCTTTTAAATTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC
AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA
TAGCAATTAACCTGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTAGAGTTCTATATTTAAAGATATA
TGTGTTTATGATTTTCTGAAATGCTTTTATAGAAATTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT
TTACATATTTGCTTCTGAACCTTGTGTTTACCTGTATCCTTTATTTACATTGGGTTTTCTTTTATAGTTTGG
TTTTTCACTCCTGTCAGTCTATTTATTATTCAAATAGGAAAAATTAATTTACAGGTTGTTTTTACTGTAGCTTAT
AATGATACTGTAGTTATTCCAGTTACTAGTTTACTGTGAGAGGCTGCCTTTTTCAATAAATATTGACATAATA
ACTGAAGTTATTTTATAAGAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGA
CTCAAAGAATCACAATTTGTGAGTAACATGATGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGTAAAAAT
CCAATCAGTCAAAGAGGTCAATGAATTAAGGCTTGCACTTTTTTCAAAAAAAAAAAAAAAAAA

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FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRD LKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLDNQGGQYESWNYRYDFGI
YDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICS NLYVFQP
SLAVFKGQGTKEYEIIHGGKILYDILAFAKESVNSHVTTLG PQNFNPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEHEYEGHHS
AEQILEFIEDLMNPSVVS LTPPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTD LTPQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDC
QAYAQT CQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLET LRNQGKRNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGG
GTCGTTGGTGAAGTTTTTCATTCCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAACCTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTACCA
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAATGAATAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACATTTTTT
TCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCCTT
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGA
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT
TCATTAGCCCAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAGTGGACCCTCTATATTTCCCTCCCTTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAAECRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV
YPADLLSTKDEEITKTTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLLID
GILTNNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

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FIGURE 193

CGGCGGCGGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCCCGGGGC
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACGTCCTTCT
CTAGGCCGACACGGGGCCGCGCTGCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACC
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCAGCCCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGACAAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCCGTGCCCATGCTGCGGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

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FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSMILLIIVYWDSAGAAHFYLHTSFSPHTGPPLPTPGPDRDRELTA
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESSVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFTPTEKRAFDDIPNSELHSHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLHLRGAPYRDPLRIPREHVHNASAHLTFNKEWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWQRQVYRLCHPCQIDYDFVGKLETLDDEAQLQLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:**Signal peptide:**

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

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FIGURE 195

TCGGGCCAGAATTCGGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCTACTGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTGATTTCTCTCATTT
CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACCTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

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FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLLDCVVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

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FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGAAGTGGCCTCACAACCTG
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCCCTGTGCGCCGCCG
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGA
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

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FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCL
GCVNPFTMQEDRSMVSPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIavgctCIF

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAACTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAAAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG
GCCGCTTCTTTGTCACTACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT
TATCGTGGCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAATT
CCTGCTTGGTGTTCTTATGTGTTTTTCGTATAGCCACCTTGTTTTTGGCCTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGATAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGGCCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCTTGCCCAGC
TGACACAGAGGTGGTGGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGAC
TGTAGATTTAATGATGCGTTTTTCAAGAATACACACCAAACAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTGTACCAAATCCTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
GACAATCAGGATATAGAAAAACAAACGTAAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTTCATTTACTTAGGGGTCAGAGAGTCTCGACCAGAGGAGGCCATTCCAGTCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCCTTTTCTTGTTGTAAGTATTTAT
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTACAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAATTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC
TACTTTAATAATAACTAAAAACCCTTCTGATTTTTCCTTCAGTGATGTGCTTTTGGTGAAA
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTGATTTTGTTCATCTTCTGTAATC
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPSCQQT DSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSE RSEQNRRSEEAHRAEQLQDAEEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAE EEEEEEDNLAAGVDEERSEANDQGPPGEDGV TRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRK SQHADKGL

Important features:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

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FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAATGAATATCATCCTGATTTAGAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACT
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG
TATGGATTACAGTGTCACTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG
TTAGAGAGCTTGGCCAACCTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT
GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTTATTTTGGAGATAGGGTCT
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCCCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
TGATCTGCCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAT
ATATTTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACCTCTA
ATTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTGCAACGG
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGT
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCTCGGCCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
TGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAAACATTTTGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCATTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG
TGCTGATTTGTCTTATTTTTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATA
TTTCTGTATTACTAGGGAGGCATTTACAGTCTCTAATGTTGATTAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTTCAT
TTCAATAAAAAAAACTCTTATCAAAAAA

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FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:**Type II transmembrane domain:**

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

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FIGURE 203

[illegible]

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FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QESLAQGPPLLATSVTSWWSPQNISLPSAASFTHSFHSPHTAAHNASVDMCELKRDQLQLL
SQFLKHHPQASRRPSAAPASQQLOSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEEQSEIMEYSVLLPRTLFRQTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTEPVVLTFOHQLOPKNVTLOCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVDVAVHKHYLSLLSYVGCVVVSALACLVTIAAYLCSRVPLPC
RRKPRDYTIKVHNMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLE
GYNLYRLVVEVFSGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFILFIWYWSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:**Signal peptide:**

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

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FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTCTTCTGTTCAACATGG

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTTGCTTTGA
TCCTTTTCAAAAAGTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCT
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCTGGCGGTGGTGAAAGAGAC
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGC
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTAAGTGTGTCTACTAATG
GAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAAATGTATGGATACAACCTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGTTCTGGTACTGTACCAG
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCCAGGGT
TCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCCAG
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAATTTGGCAACTTCTTGSCAAGGCTTTTGTTCCTTGGAA
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACTTCT
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG
GTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTACCGACGCTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCT
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
ACAGCTCTTTTGTAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTAT
TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTC
GATACGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC
TCTAAAGCTCCATGTCCTGGGCCTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACAT
ATGTAACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAGGAACATATGTTGCTATGAATTAACCTTGT
GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAATTTCTGCCATTTAGAAGAAGAGAACTACA
TTCATGGTTTGAAGAGATAAACCTGAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG
TTTCATTTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT
ATTTTTACCAAAGGTATTAAATATTCTTTTTATGACAACCTAGATCAACTATTTTGTAGCTTGGTAAATTTTTCT
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAATACATGTATTTCA
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA
GACTTTTTGAAAATAATTAAATATCATATCTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA
AAGTAGACATTCAGATCCAGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT
AAAGCACCTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGTGCTGTGCTGAGTAGGAACACATCCTATTTA
TTGTGATGTTGTGGTTTTATTATCTTAACTCTGTTCCATACACTTGATATAAATACATGGATATTTTATGTACA
GAAGTATGTCTCTTAACCAAGTTCACTTATGTACTCTGGCAATTTAAAGAAAATCAGTAAATATTTTGCTTGT
AAAATGCTTAATATNGCCTAGGTTATGTGGTGAATTTGAATCAAAATGTATTGAATCATCAAAATAAAGA
ATGTGGCTATTTTGGGGAGAAAATTAAGGATAACAGGTAATGCGGCC

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FIGURE 207

MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQ
LRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG

Signal sequence:

amino acids 1-14

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FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGAAGA
AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATCTTATCCTTTTAAACATAATCCTAATTTCC
AAACTCCTTGGGGCTAGATGGTTTCTTAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG
ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATCCCACGACACCACGAACTCACCCCTC
ACCATTAAACCACATACCAGACATCTCCCAGCGTCTTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCA
TGCAACTGTGTACCTATTCCTAGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAACCCAGAAAGC
TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCC
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC
AACATAGAAATACTCTACCTGGGCCAAAAGTGTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA
GATGCCTTCTTAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCTACTGTT
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAAGATGATTTTAAATAAC
CTCAACCAATTACAAATTTGACCTAAGTGGAATTTGCCCTCGTTGTTATAATGCCCATTTTCTTGTGCGCCG
TGTAATAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTATGCGCTGACAGAATTAAGTTTTACGTCTA
CACAGTAATCTCTTTCAGCATGTGCCCAAGATGGTTTAAAGACATCAACAACTCCAGGAATGGATCTGTCC
CAAACTTCTTGGCCAAAGAAATTTGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCAATTGGATCTG
TCTTTCAATTTTGAACCTTCAAGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG
AAAATTTCTGCGGATCAGAGGATATGTCTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA
AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAATTTGCTAACCTCAGCATGTTTAAACAATTTAAAGA
CTGAAAGTCTAGATCTTTTCACTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAT
GCCAGAATCTCTGTAGAAAGTTATGAACCCAGGTCTGGAACAATTACATTATTTAGATATGATAAGTATGCA
AGGAGTTGAGATTAACAAACAAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC
TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTTCAGCATCTTCTTCTCCTCAATGCCCTG
AATCTGTCAGGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTTCAACCTTTAGCAGAGCTGAGATATTTG
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT
CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA
ACTCTGGAAATTCAGAGGAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG
AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAATTTCCCTAAGTTTCTTGCCCTTCTGGAGTTTTTGATGGT
ATGCCCTCCAAATCTAAGAATCTCTCTTTGGCCAAAAATGGGCTCAATCTTTCACTTGGGAAGAACTCCAGTGT
CTAAGAACCTGGAACTTTGGACCTCAGCCACAACCACTGACCACTGTCCCTGAGAGATTGTTCAACTGTTCC
AGAAGCCTCAAGAATCTGATCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGCTCTC
AACATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG
GTTAACCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA
TCTGTATCTCTCTTTCTCATGGTGATGATGACAGCAAGTCACTCTATTTCTGGGATGTGTGGTATATTTACCAT
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATGTGTAT
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAAGAGAGAAA
CATTTTAATTTATGTCTCGAGGAAAGGGACTGTTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA
CAGCTTAGCAAAAAGACAGTGTGTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAAGATAGCATTTTAC
TTGTCCCATCAGAGGCTCATGGATGAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAAG
TCCAAGTTCTCAGCTCCGAAAAGGCTCTGTGGAGTTCTGTCTTGAAGTGGCCAACAACCCGCAAGCTCAC
CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCTATAGTCAAGGTGTTCAAGGAA
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCCTGGC

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FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTTNLTTLTINHIPDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYR
NPCVYSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLSKL
KILRIRGYVFKELKSFNLSPLHNLQNLVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRDLHL
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTSRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSKLNILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHNRFLCTCDAVWFVWWVNHTEVTIP
YLATDVTVCVGPAGHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIIIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACACAGAAACATGGAAAAACATGTTCCCTTC
AGTCGTCAATGCTGACCTGCATTTTCCTGCTAATATCTGTTCCCTGTGAGTTATGCGCCGAAGAAAAATTTTCTA
GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAG
TTCCCCAAACGGTGGGCAAATATGTGACAGAACTAGACCTGTCTGATAATTCATCACACACATAACGAATGAAT
CATTTCAAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAAATC
CCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCCCTCAACCTAAAAAACCTAAGGGGAGTTACTGC
TTGAAGACAACCAGTTACCCCAAATACCCCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACA
ATATATACAACATAACTARAGAGGGGCATTTCAAGACTTATAAACTTGAAAAATCTCTATTGGCCTGGAAGTGC
ATTTTAACAAAGTTTGGCAGAAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT
CACTATCTTTCAATTCTCTTTACACAGTGCACCCAACTGCCAAGCTCCCTACGCAAACTTTTTCTGAGCAACA
CCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTACTAGATTTAAGCGGGAACT
GTCCGAGGTGCTTCAATGCCCATTTCCATGCGTGCCTTGTGATGGTGGTGCCTTCAATTAATATAGATCGTTTTG
CTTTTCAAAAGCTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAAATGCTGCCTGGT
TTAAAAATATGCTCATCTGAAGGTGCTGGATCTTGAATCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCAT
TTTTAACGATGCTGCCCCGCTTAGAAATACCTGACTTGTCTTTTAACTATATAAAGGGGAGTTATCCACAGCATA
TTAATATTTCCAGAACTTCTCTAAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTGTTCCAGGAAC
TCAGAGAAGATGATTTCCAGCCCTGATGCAGCTTCCAACTTATCGACTATCAACTGGGTATTAATTTTATTA
AGCAAATCGATTTCAAACCTTTCCAAATTTCTCCAATCTGGAATTTATTTACTTGTACAGAAACAGAAATATCAC
CGTTGGTAAAGATACCCGGCAGAGTTATGCAAAATAGTTCCTCTTTTCAACGTCATATCCGGAACAGACGCTCAA
CAGATTTTGAGTTTGACCCACATTCGAACCTTTATCATTTACCCGTCCTTTAATAAAGCCACAATGTGCTGCTT
ATGGAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCAAACCAATTTGAAAATCTTCTGACA
TTGCCCTGTTTAAATCTGTCTGCAATAGCAATGCTCAAGTGTAAAGTGAAGTGAATTTTCAAGCATTCTCATG
TCAAATATTTGGATTTGACAAACAATAGACTAGACTTTGATAATGCTAGTGTCTTACTGATGCTCCGACTTGG
AAGTCTAGATCTCAGCTATAATTCACACTATTTTCAAGATAGCAGGCGTAACACATCATCTAGAATTTATTCAAA
ATTTACAAATCTAAAGTTTAACTTGGCCACAACAACATTTATACTTTAACAGATAAGTATAACCTGGAAA
GCAAGTCCCTGGTAGAATTAGTTTTAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAACAGGTATA
TCTCCATTTCAAAGGTCTCAAGAATCTGACAGCTCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAATG
AAGCATTCCTTAATTTGGCAGCGAGTCTCACTGAACATACATATAAATGATAATATGTTAAAGTTTTTAACTGGA
CATTACTCCAGCAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTTAACTGATAGCC
TATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCACCTACCTCTGGCTTTC
TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTG
AACTAAGACCACCACCAATATCTATGTTGGAATACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAG
ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAATTTCCAGACTGGTAGATGTCATTTGTGCCAGTCTCG
GGGATCAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTTCAGATGTCAGTGCAGTATATTAT
TTTTCTTACGTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACCATTTGTTTTACTGGGATGTTT
GGTTTATATATAATGTGTGTTAGCTAAGGTAAGGCTACAGGTCTCTTCCACATCCCAAACCTTCTATGATG
CTTACATTTCTTATGACACCAAGATGCCCTGTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAG
AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC
TCATGCAGAGCATCAACCAAGCAAGAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAGCTGGAACCTTA
AAACAGCTTTTTACTTGGCTTTGTCAGAGGCTAATGGATGAGAACATGGATGTGATTATTTATCCTGCTGGAGC
CAGTGTACAGCATTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCCTCCAGTGGCTGACA
ACCCGAAGGCAGAAAGGCTTGTGTTGGCAAACCTCTGAGAAATGTGCTTCTGACTGAAAATGATTACGGTATAACA
ATATGTATGTGATTCATTAAGCAATACCTAGCTGACGTTAAGTCATGATTTCCGCGCCATAATAAAGATGCAAG
GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTTATCCCAAACCTTAGTGGTTTAAACAAACACA
TTTGCTGGCCACAGTTTTTGGGGTCAGGAGTCCAGGCCAGCATAACTGGGTCTCTGCTCAGGGTGTCTCAG
AGGCTGCAATGTAGGTGTTACACAGAGACATAGGCATCACTGGGGTCACACTCATGTGGTTGTTTTCTGGATTCA
ATTCCTCCTGGGCTATTGGCCAAAGGCTATACCTATGTAAGCCATGCGAGCCTCTCCCAAGGCAGCTTGCTTC
ATCAGAGCTAGCAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAAATCGAATCAAAAAGTGAT
ATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAACACAGGTCCCACAGCTCCATGGGAGTGACCACC
TCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGATTGCTTCAGTTGGTCATCAACTATTTCCCT
TGACTGCTGTCTGGGATGGCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGAGGGATCACTGTGGACC
ATCTTAGCAGTTGACCTAACACATCTCTTTTCAATATCTAAGAATTTTGCCACTGTGACTAATGGTCTTAATA
TTAAGCTGTTGTTTATATTATATATCTATGCTACATGGTATGCTTATATTATGCTGTGGTTCGGTTTTAT
TTACAGTTGCTTTTACAAATATTTGCTGTACATTTGACTTCTAAGGTTTAGATGCCATTTAAGAAGTGAAGTGG
ATAGCTTTTAAAGCATCTTTACTTCTTACCATTTTTTAAAGTATGCAGCTAAATCGAAGCTTTTGGTCTATA
TTGTTAATTGCCATTGCTGTAAATCTTAAATGAATGAATAAAATGTTTCATTTTACAAAAA

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FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQND SVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHQN GNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSTIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKFLSNTQIKYISEEDFKGLINL
TLDDLSGNCPRCFNAPFPCVPCDGGASINIDREAFQNL TQLRYLNLSSTSLRKINA AWFKNM
PHLKVLDLEFN YLVGEIVSGAFLTMLPRLEILDLSFN YIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQLPNLSTINLGINF IKQIDFKLFQNF SNLEIIYLSENRISPLV
KDTRQSYANSSSFQRHIRKRRSTD FEFDPHSNFYH FTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACNLNSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELS DLEV
LDLSYN SHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYT LTDKYNLESKSLVELVFSGNRL
DILWNDDDNRYISIFKGLKNLTRLDSLNLRLKHIPNEAFLNLPASLTE LHINDNMLKFFNWT
LLQQFPRLLELDLRGNKLLFLTDSLSDFTSSSLRTL LLSHNRISHLP SGFLSEVSSLKHL DLS
SNLLKTINKSALETKT TTKLSMLELHG NPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFIT TMVMLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQT FYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWD PGLAIID
NLMQSINQSKKT VFLTKKYAKSWNFKTA FYLALQRLMDENMDV IIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 212

CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCCGTGTCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCACCTCCTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTG
GAGGAGCAGCTGGGGTCTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSDGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTTCAGCTTGGCTGGGCCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGCCCCGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCC**ATG**AGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCCG
TGCAGCGTGTGTACCAGCCCTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCTGGGGTCTCTGCTCCTGCAAGAAAGA
CTCG**TGA**CTGCCCAGCGCTCCAGGCTGGACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCCAATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACATAAAAATGAAACGTG

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

276/237

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCT
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAAATAAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPGGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

FIGURE 218

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGT CAGGAGGAGACAGCCTCCCGGCCCGGGGAG
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCTGGGACGGTCCGTTTCTGCCGT CAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGG
AGATTGCTCTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGTAATCGCAAAACCCATTTTGAGCAGGAATCCAATCA
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAACTCC CAGGCAGGAACACCTTTTGCTGTG
ATGGCCCGCTCATGATGGCCCCGGCAAAAGGGCATTCTTCTACCTGACCCCTTTTCTCATCTCTGGGGACATGTACAC
TCTTCTTCGCCCTTTGAGTGCCGCTACCTGGCTGTT CAGCTGTCTCTGCCATCCCTGTATTTGCTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACCACTT CAGTGACCTGGAGTGATTCTCGGGCGCTACCCAGATG
AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCTCGTA
TCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC
GGGCCCTCCCATTTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTGTG
TTGGAAAGAGGAACCTACCGTACTTCTACCTCTCATCCTTTCTCTCTCCCTCCTCACAATCTATGCTTCCGCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAGAACTCCTGGAACTG
TTCTAGAAGTCTCTATTGCTTCTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCATACTTTCTCGTGG
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA
TTTTGCCACTGGAGGAAAGTGAAGTCGACCTCC CAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAG**TAG**CCTATCTATGGAAGAGACTTTTGTGTTGTGTT
TAATTAGGGCTATGAGAGATTT CAGGTGAGAAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTCTTTGGTCTTTTAGTCACCCAGTTGCACACTGGCATTCTTCTGCTGCAAGCTTTTTTAAATTTCTGAACT
CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
CCATGGCCTCAGCCACAGGGTCCCCCTTGGACCCCTCTCTTCCCTCCAGATCC CAGCCCTCCTGCTTGGGGTCAC
TGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTCTCTGGCCACCAAGTGCCAGCATTGCCCACAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTTGTTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGT TTTTCTTTTACTCCTGCTCCCATAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACCTTGGTCACTTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC
ACTATCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCCGATGTACCCTCAAAAAAAAAAAAAATGCTAACCAGTTCTTCCATTAAGCCT
CGGCTGAGTGAGGGAAGCCAGCACTGCTGCCCTCTCGGGTAACCTACCCCTAAGGCCTCGGCCACCTCTGGCT
ATGGTAACCACACTGGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCC CAGAGCCACTT
CACCTTGGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTT CAGGGAAGAAGATTTATGT
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
GCGGTGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAAGGCGATTAAACTGTGTCTAATGCA

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FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL
FILSLSLTLTIYVFAFNIVYVALKSLKIGFLETCLKETPGTVLEVLI CFFTLWSVVGLTGFHTF
LVALNQT TNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 220

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTGTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACCTACACTTGGCTGGCTCCAACAAGCTGGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

FIGURE 222

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKG VKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Signal peptide:

amino acids 1-28

FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACGCGCTGGCCCGACTCCACCATGAACGTGCGGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
AAGGGGACAAGACAGCTGTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCACAGCACCTGCCTTACA
GAGGCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC
CAGTTCTCTGTGGGGGCTGGATTCCGAGGAACCCCTGCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAACACACCACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCCATCTTACCCTCTACATCAGTCCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACCACTGCTGGGCTCTTCTGCCCTCTCGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAAGTGGGGATGCTGCTGGGTGGGCGGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGGCCAGGACCAGCGGGCGGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTT
CTGTCTTTCTTGCTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTCAAGCTCATCAACCGCACGGAACCAAGCATCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAG
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACCTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
CCTCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC
GTCTTCCCCGCTGGCATCCTGCAGGCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACCTCGGTGGCATC
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG
CGGCCCTGGTGGCAGATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACACGGGGGGCTGAAG
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACAGCTCTTCTTCTGGGATTGGCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGG
CACTTCGGCTGCCCTGTGGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACCTGGGCGAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG
TGCTCTGCTTTGGGGGTGCCCTGCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTACCCCT
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCTATAGGAAGGAGTCTGCC

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FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTA
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMNLNLYNFSKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLA AFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGS PMNPGQLCEVW

Type II Transmembrane domain:

amino acids 32-57

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FIGURE 226

GCCCCGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCGCTCCCGCGCCCTCCTCCCTCCCTCCTCCC
CAGCTGTCCCGTTTCGCGTCATGCCGAGCCTCCCGGCCCGCCCGGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCT
CGGCTCCCGGCCCGGCCCGGCCCGGCCAGAGCCCCCGTGTGCTGCCATCCGTTCTGAGAAGGAGCCGCTGCC
CGTTCCGGGGAGCGGCAGGTAGGTGGCGGCCCGGGGGAGGCCCGGCCCGGGGAGTCCGGGCTCGGGGCGAGTCAGCGC
CAGCCCCGAGGGGGCGCGGGGGCGCAGGTGGCTCGGCGCGGCCGGGCCCGGAGGGTGGGCGGGGGCAGAAGGGC
GCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGGGCGGCACACGGCGCGAGCTGGGCAGCGGCCCTCCAGC
CAAGCCCCGTCCCCGAGGCTGCACCTTCGGCGGGAAGGTCTATGCCTTGACGAGACGTGGCACCCCGGACCTAGG
GGAGCCATTCCGGGTGATGCGCTGCGTGTGTGCGCTGCGAGGCGCAGTGGGGTCCCGCTACAGGGGGCCCTGG
CAGGGTCAGCTGCAAGAACATCAAAACCAGAGTGCCCAACCCCGGCCCTGTGGGCAGCCGCGCCAGCTGCCGGGACA
CTGCTGCCAGACCTGCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTGCGAGGCGGTGGCACGAGCCCCG
AGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCTGGACCGCCCTACAGGATCCGCTT
CTCAGACTCCAATGGCAGTGTCTGTGTTGAGCACCTGCGAGCCCCACCAAGATGGCCTGGTCTGTGGGGTGTG
GCGGGCAGTGCCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCA
CCCTTCAGGGGAGGTCTGGGGGCCCTCTCATCCGGCACCGGGCCCTGTCCCGAGAGACCTTCAGTGCCATCTGAC
TCTAGAAGGCCCCACCAGCAGGGCGTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGACTCCTTGCA
TTTTTTGCTGCTCTCCGAGGCCCTTGCAAGACTAACCAGGTTCCCTTGAGGCTCCAGATTCTACACAGGGGCA
GCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCAGGAACAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGT
CCAGGAGATGGACTGGCTGGTGTGCTGGGGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCAT
CAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGTCCCTGCAAAAGTGTCTTTGTGGGGCTAATGCCCTGATCCC
AGTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCTGATCCTCCAGGTGCAATT
GGTAGGGACAACCACTGAGGTGGTGGCCATGACACTGGAACCAAGCCTCAGCGGAGGGATCAGCCCACTGTCTT
GTGCCACATGGCTGGCTATCCTCCCTGCCCGCAGGCCGTGGGTATCTGCCCTGGGCTGGGGTGCCCGAGGGGGC
TCATATGCTGCTGCGAATGAGCTCTTCTGAACGTGGGCACCAAGGACTCCCAGACGGAGAGCTTCGGGGGCA
ACGTGGCTGCCCTGCCCTACTGTGGGGCATAGCGCCCGCTGCCCGTGCCCGTAGCAGGAGCCCTGGTGCTACC
CCCTGTGAAGAGCCAAGCAGCAGGGCAGCCTGGCTTTCTTGGATACCCACTGTACCTGCACCTATGAAGTGCT
GCTGGCTGGGCTTGGTGGCTCAGAACAGGCACCTGTCACTGCCACCTCCTTGGGCCTCCTGGAACGCCAGGGCC
TCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAGGCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAATGCTGCG
GCACCTGGCAAAAGGCATGGCTTCCCTGATGATCACCACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGGAGCCT
CTCCTCCAGGTGACATAGCCAACCAATGTGAGGTTGGCGGACTGCGCTGGAGGCGGGCGGGCGGAGGGGGT
GCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCCG
CAAACCTGGTGGTCTGGGCGGCCCGGAGACCCCAACACATGCTTCTTCGAGGGGCGAGCAGCGCCCCACGGGGC
TCGCTGGGCGCCCACTACGACCCGCTCTGCTCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGT
GGTGTGCCCCACCGCCAGCTGCCCCACCCGGTGACGGCTCCCGACCACTGCTGCCCTGTTTGGCTGGCTGCTA
TTTTGATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCAGCCCGTTGTGCCCGCTTTGGCTTAATTAA
GTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCACTGTCCCCGGCTGGC
CTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAACAGTGTCCAGGTGAGGCCACCCCGAGCTGGG
GGACCCCATGCAGCTGATGGGCCCGGGGCTGCCGTTTGTGTTGGGAGTGGTCCCAGAGAGTCAGAGCTGGCA
CCCCCTCAGTGCCCCCGTTTGGAGAGATGAGCTGTATCCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGT
GTGAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGAGCTTCCAGGGAGGTCCCTGAAGAAGCTGAAGGTCA
CTGTGTCCAGTGCCCTCTGGGGGACACTCAGTGTCTGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTTCCCGCTGCACGGCCACC
GGCGGCGTAAGTGAGGGAGTCCAGGGTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAG
GGAAGGGAGCACTCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAACTCACAGCA
ACCTGGTGGAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGAAATTAAGCAACGAG
ATGAAGGTCAACCCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGCCTTTCTGGGACCAAGGCAGGGATGCTT
TGCCCTGCCCTCTATGCCTCTCTGTGCTCTCCACTCCCTCTCCCTCCTCAACATTCCCTCCCTTCTGTCTCC
AGCAGCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCC
AAGTGACCAAGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCAATTCCTGTGGGAAG
CCAGTGCCCTTTGCTCCTCTGTCTGCTCTACTCCACCCCACTACCTCTGGGAACACAGCTCCACAAGGGG
GAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCTGCCCTGCCACCTCGGCCCTGTCTCTGGAA
GCCCCACCCCTTTCTTCTGTACATAATGTCACTGGCTTGTGGGATTTTAATTTATCTTCACTCAGCACCAG
GGCCCCGGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTGTATTATTAAAC
ATTTCTTTTTCAGTCTTTGGGCATGAGGTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCCTGGTGGACAAGGG
GCNAGAGTAGGAGGTGAGAGAGAGGAGCTGTGACACTTGGGGAGCTGAAGAGACCTGGAGAGGCAGAGGATAG
CGTGGCNCNTTGGCTGGCATNCCTGGGTTCGCGCAGAGGGGCTGGGGATGGTCTTGTGAGATGGTCTAGAGACTCAAG
AATTTAGGGAAGTAGAAGCAGGATTTTGACTCAAGTTTAGTTTCCACATCGCTGGCCTGTTTGTGACTTTCATG
TTTGAAGTTGCTCCAGAGAGAGAATCAAGGTGTACCAGGCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTTCT
TTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC

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FIGURE 227

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC
TCCACCATGAACGTGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTGGA
GGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAACTGCCCT
CCTTTCTTTCTTCTTTTCTTCCCTCCCTCCCTCCCTTTCTTCCCTTTTCTTCCCTTCCCTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTTCAGTGTGATGGGTTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCCCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

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FIGURE 228

ATGCCTACTACCTTCCAATAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCCGAACCAACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTGGGTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGGCTGGGTCTAGTCCCTCCCCCCCCACA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCCCT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCCCTCACGGGCTACCCCCACCTCACCCCTGTGCTCCTTGTGCCACTGCTCCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA
GGAGGGGAGGCAAAAACACCGAAAAACAAAAGAGAGAAACAACACCCAACAACCTGGGGTGG
GGGGAAGAAAGAAAGAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG
TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG
CTGTTGGTGCAGGGTGCTTGTGCTCGAACCAGTGGCTGGCGGCGGTGCTCCTCAGCCTGTG
CTGCCTGCTACCCTCCTGCCTCCCGGGCTGGACAGAGTGTGGACTTCCCCCTGGGCGGCCGTGG
ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT
TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTGCGGGAGGTGATAAGTGGTCAGT
GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG
TAGATGTGACAGATGATGGCCATACACGTGTTCTGTTTCACTCAACATACACCCAGAACA
ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC
CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACCAGAGCCTTCCA
TTTCTTGGCGACACATCTCCCCATCAGCAAAACCATTTGAAAATGGACAATATTTGGACATT
TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCAGGAAATGCTGTGTCAAT
CCCAGATGTGAGGAAGTAAAGTTGTTGTCAACTTTGCTCCTACTATTGAGGAATTAAT
CTGGCACCGTGACCCCGGACGCGAGTGGCCTGATAAGATGTGAAGGTGCGAGGTGTGCCCT
CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT
TCAAAATTTTAGCACAAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA
ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCCT
CCAAGTACAGCCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT
TGTGTTGACACTGTCCTCTTTCACCAGCATATTCTACCTGAAGAATGCCATTCTACAAATAA
TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT
GGTACAGTTTGTATAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC
TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTTTGTATTAGCTACATTA
CCTTGTGAAGCAGTACACATTGTCCTTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTAG
AGGATATTAATTGTGATTTTCATGTTTGTAACTTACAACTTTTCAAAGCATTCAGTCATGGT
CTGCTAGGTTGCAGGCTGTAGTTTACAAAACGAATATTGCAGTGAATATGTGATTCTTTAA
GGCTGCAATACAAGCATTCAAGTTCCTGTTTCAATAAGAGTCAATCCACATTTACAAAGATG
CATTTTTTTCTTTTTTGTATAAAAAGCAATAATATTGCCTTCAGATTATTTCTTCAAAATA
TAACACATATCTAGATTTTTCTGCTTGATGATATTCAAGGTTTCAGGAATGAGCCTTGTAAT
ATAACTGGCTGTGCAGCTCTGCTTCTCTTTCCTGTAAGTTCAGCATGGGTGTGCCTTCATAC
AATAATATTTTTCTCTTTGTCTCCAACTAATATAAAATGTTTTGCTAAATCTTACAATTTGA
AAGTAAAAATAAACCAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC
TATTGGACTGTAAAAATCTCTTCCCTGCACTGACAATGGGGTTTGAGAATTTTGGCCCACT
AACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTC
TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCCTTTAAATGACAGCACA
GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCTTCACTAGTCCAAGCCAAAAA
TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCTTATCACCTAATATTACAAGAGTTGGTA
AGCGCTCATATTAATTTTATTTTGTGGCAGGTATTATGACAGTGCACCTGGAGGGTATGGA
TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC
AGGAGGAAATTACAGAGACAATTATGACAACCTGAAATGAGACATGCACATAATATAGATACA
CAAGGAATAATTTCTGATCCAGGATCGTCCCTTCAAATGGCTGTATTTATAAAGGTTTTTGG
AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATGACCTGCCA
AGGTAGCTGAAGACCTTTTAGACAGTTCCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA
AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 230

MMLLVQGACCSNQWLAAVLLSLCCLLPSCLPAGQSVDFPWAAVDNMMVRKGD TAVLR CYLED
GASKGAWLNRSSIIIFAGGDKWSVDPRVSISTLNKR DYS LQIQNV DVTDDGPYTCSVQTQHTP
RTMQVHLTVQVPPKIYDISNDMTVNEG TNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYECSAENAVSFDPVRKV KVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGIIIIQN FSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL
NPPSTAQYGITGSADVL FSCWYLVLTLS SFTSIFYLKNAILQ

Important features of the protein:**Signal peptide:**

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325**Myelin P0 protein:**

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
GCGGCTCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG
CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT
AGACAACCTTCACTCAGAACCCAGGGATGTTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTC
TTCAAGGTCACAAGGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCGCCGGGACCACCTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAAGGTGCTCCAGGGAAGCAAG
GAGCCACTGGCACCCCAAGGAGAGAGAGGGCAGCAAAGGCGATGGGGGTCTCATT
GGCCCCAAAAGGGGAACTGGAATAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGAGGGCCTCCTGGAGCCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCGGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGC
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG
GCTGGCAGGTCCCAAGGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC
GTCAGGATTGTGCGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTCAGTGTGCGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA
TGAATGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTTGACCCCGGAACCCCTTTCA
CTTCTCTGCTCCCGAGGTGTCCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAGCTCAACATCATTGA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPF EINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVDNFTQNP GMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGPSGPQGP PGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE
KGD LGLPGSKGDRGMKG DAGVMGPPGAQGSKGD FGRPGPPGLAGFP GAKGDQGPGLQGVPG
PPGAVGHPPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGD TGLQGGQGRKGESGVPGPA
GVKGEQGS PGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWL DNVQCRGTESTLW
SCTKNSWGHHD CSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGGCCAACTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAACTGATGGTACTTGTTTTTCAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG
TGATTCCTTGCAACAATCAATTGAAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTC
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLG VQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG

KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCCAGGTCTGGAGCGAATTCACAGCCTGCAGGG
CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC
GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATG
TGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCCGCGCTGGCTGTG
CGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCCTCTTCGGGTGGTTTA
TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT
GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC
AGGAACAGAACAAAACCTTTCAGCTTGCAAAGCAAATTCATCCCAGTGGAAGAATTTGGCC
TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCTACCCAAATAAGACTCATCCC
AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTGAACC
ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTTCTCTCCTC
AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAAGTGAAGACTTCTTTAAA
TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGT
TTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT
CCGACCCTGCTGACTACTTTGCTCCTGGGGTGAAGTCTTATCCAGACGGTTGGAATCTTCTCCT
GGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCCTCTCACACC
AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGAATTCAGAGGGCTGTTGGTCTTCCAA
GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC
TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
CTTTACTGGAACTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATT
CTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT
TGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA
CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA
GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
AGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC
TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG
ACTAAAAAAGTCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAAGCAAATTTGGGATCTGG
AAATGATTTTGTAGGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA
AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT
GAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCAGGTTTCG
AGGAGGGATGGTGTGTTGAGCTAGCCAATTCCATAGTGTCTCCCTTTTGATTGTGAGATTATG
CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
ATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT
TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA
TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTTATTGATCCATTAGGGTTACCAGAC
AGGCCTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC
ATCCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCT
GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACT
TTGAGTGAAGTAGCCCTAAGAGGATTTTTTAGAGAAATCCGTATTGAATTTGTGTGGTATGTCA
CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTGAAATAAAGT
TGAATATTATATATAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRRPRLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFI
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH
PNYISIINEDGNEIFNTSLFEP PPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSGKIVIRYGVFRGNKVKNALAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQQRGNILNLNGAGDPLTPGYPANAYRRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDYV
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLQLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYES
WTKKSPSPFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDLSFSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSH NKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713

(19) World Intellectual Property Organization
International Bureau



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14 September 2000 (14.09.2000)

PCT

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16/28, G01N 33/68, 33/543, A61K 47/48, 51/08, 38/17

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PCT/US99/28551	2 December 1999 (02.12.1999)	US
PCT/US99/28565	2 December 1999 (02.12.1999)	US
PCT/US99/30095	16 December 1999 (16.12.1999)	US
PCT/US99/31243	30 December 1999 (30.12.1999)	US
PCT/US99/31274	30 December 1999 (30.12.1999)	US
PCT/US00/00219	5 January 2000 (05.01.2000)	US
PCT/US00/00277	6 January 2000 (06.01.2000)	US
PCT/US00/00376	6 January 2000 (06.01.2000)	US

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(74) Agents: KRESNAK, Mark, T. et al.; Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080-4990 (US).

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[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.



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(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/04341

A. CLASSIFICATION OF SUBJECT MATTER					
IPC 7	C12N15/12	C12N15/63	C12N5/10	C12N1/21	C12N1/19
	C07K14/47	C07K14/705	C07K19/00	C07K16/18	C07K16/28
	G01N33/68	G01N33/543	A61K47/48	A61K51/08	A61K38/17
According to International Patent Classification (IPC) or to both national classification and IPC					
B. FIELDS SEARCHED					
Minimum documentation searched (classification system followed by classification symbols)					
IPC 7 C12N C07K G01N A61K					
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched					
Electronic data base consulted during the international search (name of data base and, where practical, search terms used)					
C. DOCUMENTS CONSIDERED TO BE RELEVANT					
Category *	Citation of document, with indication, where appropriate, of the relevant passages				Relevant to claim No.
X	WO 98 57983 A (ZYMOGENETICS INC) 23 December 1998 (1998-12-23) the whole document				1-3, 5-13, 15-21
A	KLEIN R D ET AL: "Selection for genes encoding secreted proteins and receptors" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, US, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, no. 93, 1 July 1996 (1996-07-01), pages 7108-7113, XP002077277 ISSN: 0027-8424 the whole document				
- / - -					
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex.					
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "&" document member of the same patent family					
Date of the actual completion of the international search			Date of mailing of the international search report		
20 July 2000			18. 10. 00		
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016			Authorized officer Smalt, R		

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/04341

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	YOKOYAMA-KOBAYASHI M ET AL: "A signal sequence detection system using secreted protease activity as an indicator" GENE,NL,ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, vol. 163, no. 2, 3 October 1995 (1995-10-03), pages 193-196, XP004041983 ISSN: 0378-1119 the whole document ---	
A	EP 0 834 563 A (SMITHKLINE BEECHAM CORP) 8 April 1998 (1998-04-08) the whole document ---	
A	WO 97 07198 A (GENETICS INST) 27 February 1997 (1997-02-27) the whole document ---	
P,X, L	WO 99 46281 A (BAKER KEVIN P ;CHEN JIAN (US); GENENTECH INC (US); GURNEY AUSTIN () 16 September 1999 (1999-09-16) whole document, particularly the passages referring to PR0213 (e.g. pages 2,50,123,183), and the claims ---	1-3, 5-13, 15-21
P,X	WO 99 54437 A (MILLENNIUM BIOTHERAPEUTICS INC) 28 October 1999 (1999-10-28) the whole document -----	1-3, 5-13, 15-21

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/04341

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Invention 1 : claims 1-3, 5-13, 15-21, all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Invention 1: claims 1-3,5-13,15-21, all partially

Nucleic acid with seq.ID.1, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.2 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.2 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide.

Invention 2: claims 1-29,38-43, and 50-53,
all partially

Nucleic acid with seq.ID.611, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.612 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.612 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PR0337 (seq.ID.523) using its interaction with PR04993 (seq.ID.612), method for linking a bioactive molecule to a cell expressing PR0337 through the use of PR04993, and method of modulating at least one activity of said cell thereby.

Invention 3: claims 1-29,38-43, and 50-53,
all partially

Nucleic acid with seq.ID.522, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.523 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.523 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PR04993 (seq.ID.612) using its interaction with PR0337 (seq.ID.523), method for linking a bioactive molecule to a cell expressing PR04993 through the use of PR0337, and method of modulating at least one activity of said cell thereby.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Invention 4: claims 1-21,30-37,44-49, and 54-57,
all partially

Nucleic acid with seq.ID.613, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.614 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.614 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PRO700 (seq.ID.523), PRO725 (seq.ID.616) and/or PRO739 (seq.ID.618) using their interaction with PRO1559 (seq.ID.614), method for linking a bioactive molecule to a cell expressing PRO700, PRO725 or PRO739 through the use of PRO1559, and method of modulating at least one activity of said cell thereby.

Invention 5: claims 1-21,30-37,44-49, and 54-57,
all partially

Nucleic acid with seq.ID.89, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.90 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.90 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PRO1559 (seq.ID.614) using its interaction with PRO700 (seq.ID.90), method for linking a bioactive molecule to a cell expressing PRO1559 through the use of PRO700, and method of modulating at least one activity of said cell thereby.

Invention 6: claims 1-21,30-37,44-49, and 54-57,
all partially

Nucleic acid with seq.ID.615, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.616 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.616 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

PR0381, as represented by seq.ID's 144 and 145,
PR0386, as represented by seq.ID's 149 and 150,
PR0540, as represented by seq.ID's 156 and 157,
PR0615, as represented by seq.ID's 161 and 162,
PR0618, as represented by seq.ID's 168 and 169,
PR0719, as represented by seq.ID's 177 and 178,
PR0724, as represented by seq.ID's 182 and 183,
PR0772, as represented by seq.ID's 189 and 190,
PR0852, as represented by seq.ID's 195 and 196,
PR0853, as represented by seq.ID's 205 and 206,
PR0860, as represented by seq.ID's 210 and 211,
PR0846, as represented by seq.ID's 215 and 216,
PR0862, as represented by seq.ID's 220 and 221,
PR0864, as represented by seq.ID's 225 and 226,
PR0792, as represented by seq.ID's 230 and 231,
PR0866, as represented by seq.ID's 235 and 236,
PR0871, as represented by seq.ID's 244 and 245,
PR0873, as represented by seq.ID's 253 and 254,
PR0940, as represented by seq.ID's 258 and 259,
PR0941, as represented by seq.ID's 263 and 264,
PR0944, as represented by seq.ID's 269 and 270,
PR0983, as represented by seq.ID's 283 and 284,

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PR01057, as represented by seq.ID's 295 and 296,
PR01071, as represented by seq.ID's 300 and 301,
PR01072, as represented by seq.ID's 302 and 303,
PR01075, as represented by seq.ID's 308 and 309,
PR0181, as represented by seq.ID's 321 and 322,
PR0195, as represented by seq.ID's 329 and 330,
PR0865, as represented by seq.ID's 336 and 337,
PR0827, as represented by seq.ID's 345 and 346,
PR01114, as represented by seq.ID's 351 and 352,
PR0237, as represented by seq.ID's 357 and 358,
PR0541, as represented by seq.ID's 362 and 363,
PR0273, as represented by seq.ID's 369 and 370,
PR0701, as represented by seq.ID's 374 and 375,
PR0704, as represented by seq.ID's 379 and 380,
PR0706, as represented by seq.ID's 384 and 385,
PR0707, as represented by seq.ID's 389 and 390,
PR0322, as represented by seq.ID's 394 and 395,
PR0526, as represented by seq.ID's 399 and 400,
PR0531, as represented by seq.ID's 404 and 405,
PR0534, as represented by seq.ID's 409 and 410,
PR0697, as represented by seq.ID's 414 and 415,
PR0717, as represented by seq.ID's 419 and 420,
PR0731, as represented by seq.ID's 424 and 425,
PR0218, as represented by seq.ID's 429 and 430,
PR0768, as represented by seq.ID's 436 and 437,
PR0771, as represented by seq.ID's 441 and 442,
PR0733, as represented by seq.ID's 446 and 447,
PR0162, as represented by seq.ID's 451 and 452,
PR0788, as represented by seq.ID's 453 and 454,

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PRO1008, as represented by seq.ID's 455 and 456,
PRO1012, as represented by seq.ID's 458 and 459,
PRO1014, as represented by seq.ID's 463 and 464,
PRO1017, as represented by seq.ID's 465 and 466,
PRO474, as represented by seq.ID's 467 and 468,
PRO1031, as represented by seq.ID's 469 and 470,
PRO938, as represented by seq.ID's 471 and 472,
PRO1082, as represented by seq.ID's 476 and 477,
PRO1083, as represented by seq.ID's 482 and 483,
PRO200, as represented by seq.ID's 487 and 488,
PRO285, as represented by seq.ID's 495 and 496,
PRO286, as represented by seq.ID's 497 and 498,
PRO213-1, as represented by seq.ID's 505 and 506,
PRO1330, as represented by seq.ID's 507 and 508,
PRO1449, as represented by seq.ID's 509 and 510,
PRO298, as represented by seq.ID's 514 and 515,
PRO403, as represented by seq.ID's 525 and 526,

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/04341

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